

PF 05-SEP-1996; 96WO-US14324.  
 XX  
 PR 06-SEP-1995; 95US-0523894.  
 XX  
 PA (IDEC-) IDEC PHARM CORP.  
 XX  
 PI Hanna N, Newman RA, Refl ME;  
 XX  
 DR WPI; 1997-201913/18.  
 XX  
 DR N-PSDB; AAT62870.  
 XX  
 PT Chimeric antibody comprising monkey variable domains and human  
 PT constant domains - affects CD4-mediated immune functions, esp.  
 PT useful for treatment of autoimmune disease, e.g. rheumatoid  
 PT arthritis  
 XX  
 XX  
 PS Claim 6; Page 91-93; 155pp; English.  
 XX  
 CC 3 Polypeptides (AAW14925-27) respectively comprise the heavy chain  
 CC regions of human gamma-4, gamma-4E carrying an L236E mutation in  
 CC the hinge region, and gamma-4PE carrying L236E and S229P mutations.  
 CC They can be incorporated into novel monoclonal and chimeric  
 CC antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in  
 CC which the human IgG4 Fc binding domain framework is combined with  
 CC the antigen binding domains (see also AAW14922-23) of macaque anti-  
 CC human CD4 monoclonal antibody E9.1. These antibodies show high  
 CC affinity to human CD4, have little or no immunogenicity in humans  
 CC and show reduced or absence of effector function. The gamma-4E and  
 CC -4PE mutations confer activity enhanced stability and eliminate  
 CC depleting activity. The antibodies can be used to treat autoimmune  
 CC diseases such as rheumatoid arthritis.  
 XX  
 SQ Sequence 467 AA;  
 Query Match 82.0%; Score 2112.5; DB 18; Length 467;  
 Best Local Similarity 84.5%; Pred. No. 7.8e-119;  
 Matches 402; Conservative 24; Mismatches 41; Indels 9; Gaps 2;  
 QY 1 MKHLWFFLLVAAPRWLVLSQVQLQWGGEGLLQPSSETLSRTCVVSGSGISGYVYWTIRQT 60  
 DB 1 MKHLWFFLLVAAPRWLVLSQVQLQWGGEGLLQPSSETLSRTCVVSGSGISGYVYWFIRQS 60  
 QY 61 PGKLEWIGHYICNGATTNYPNLSKRVITISKDTSKNQFFLNLSVTDADTAVVYCARGP 120  
 DB 61 PGKLEWIGHYICNGATTNYPNLSKRVITISKDTSKNQFFLNLSVTDADTAVVYCARGP 120  
 QY 121 RPDCTTICYGWVDVGMGDLVTVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFP 180  
 DB 118 ---SNILKYLHLLYWGQGVLTVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFP 174  
 QY 181 EPTVSVNNSGALTSGVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 240  
 DB 175 EPTVSVNNSGALTSGVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 234  
 QY 301 EVKFNWYVDGVEVFNHAKTKPREQYNSTRVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360  
 DB 292 EVQFNWYVDGVEVFNHAKTKPREQYNSTRVSVLTVLHQDWLNGKEYKCKVSNKALPAP 351  
 QY 361 LKTSKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420  
 DB 352 LKTSKAKGQPREPOVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 411  
 QY 421 KTTTPVLDSDGFFLYSKLTVDKSRWQQGNFVSCSVWMEALHNHYTQKSLSLSPGK 476  
 DB 412 KTTTPVLDSDGFFLYSKLTVDKSRWQQGNFVSCSVWMEALHNHYTQKSLSLSPGK 467  
 RESULT 14  
 AAW14925

AAW14925 standard; Protein; 467 AA.  
 AAW14925;  
 18-OCT-1997 (first entry)  
 Human gamma-4 heavy chain.  
 CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;  
 cynomolgus monkey; autoimmune disease; rheumatoid arthritis;  
 leukaemia; lymphoma; graft-versus-host disease; asthma;  
 transplant rejection; HIV; therapy; CE9 gamma 4.  
 Homo sapiens.  
 WOS9709351-A1.  
 13-MAR-1997.  
 05-SEP-1996; 96WO-US14324.  
 06-SEP-1995; 95US-0523894.  
 (IDEC-) IDEC PHARM CORP.  
 Hanna N, Newman RA, Refl ME;  
 WPI; 1997-201913/18.  
 N-PSDB; AAT62868.  
 Chimeric antibody comprising monkey variable domains and human  
 constant domains - affects CD4-mediated immune functions, esp.  
 useful for treatment of autoimmune disease, e.g. rheumatoid  
 arthritis  
 Claim 6; Page 82-84; 155pp; English.  
 3 Polypeptides (AAW14925-27) respectively comprise the heavy chain  
 regions of human gamma-4, gamma-4E carrying an L236E mutation in  
 the hinge region, and gamma-4PE carrying L236E and S229P mutations.  
 They can be incorporated into novel monoclonal and chimeric  
 antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in  
 which the human IgG4 Fc binding domain framework is combined with  
 the antigen binding domains (see also AAW14922-23) of macaque anti-  
 human CD4 monoclonal antibody E9.1. These antibodies show high  
 affinity to human CD4, have little or no immunogenicity in humans  
 and show reduced or absence of effector function. They can be used  
 to treat autoimmune diseases such as rheumatoid arthritis.  
 SQ Sequence 467 AA;  
 Query Match 81.9%; Score 2111.5; DB 18; Length 467;  
 Best Local Similarity 84.5%; Pred. No. 8.9e-119;  
 Matches 402; Conservative 24; Mismatches 41; Indels 9; Gaps 2;  
 QY 1 MKHLWFFLLVAAPRWLVLSQVQLQWGGEGLLQPSSETLSRTCVVSGSGISGYVYWTIRQT 60  
 DB 1 MKHLWFFLLVAAPRWLVLSQVQLQWGGEGLLQPSSETLSRTCVVSGSGISGYVYWFIRQS 60  
 QY 61 PGKLEWIGHYICNGATTNYPNLSKRVITISKDTSKNQFFLNLSVTDADTAVVYCARGP 120  
 DB 61 PGKLEWIGHYICNGATTNYPNLSKRVITISKDTSKNQFFLNLSVTDADTAVVYCARGP 120  
 QY 121 RPDCTTICYGWVDVGMGDLVTVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFP 180  
 DB 118 ---SNILKYLHLLYWGQGVLTVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFP 174  
 QY 181 EPTVSVNNSGALTSGVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 240  
 DB 175 EPTVSVNNSGALTSGVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKV 234  
 QY 241 DKXAPKSCDKTHTCPPCPAPPELLGSGPVFPPLPKPKDTLMISRTPEVTCVVDVSHEDP 300

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Db 117 -----GGAAAFDYGQGTTLTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKD 167
Qy 178 YFPEPVTWNSGALTSVHTTTPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHNKPSN 237
Db 168 YFPEPVTWNSGALTSVHTTTPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHNKPSN 227
Qy 238 TKVDKKAEPKCDKTHTCPCPCAPPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSH 297
Db 228 TKVDKTKVERKCCVE---CPCPCAPP-VAGPSVFLFPKPKDTLMISRTPEVTCVVDVSH 283
Qy 298 EDPVKFNMYVDGVEVHNKAKTPREEQNSTYRVSVLTVLHQDMLNGKEYCKVSNKAL 357
Db 284 EDPVKFNMYVDGVEVHNKAKTPREEQNSTYRVSVLTVLHQDMLNGKEYCKVSNKAL 343
Qy 358 PAPIKTIKAKQPREQVYTLPSRDELTKNOVSCLTKVKGFPSPDIAVWESNGQPE 417
Db 344 PAPIKTIKAKQPREQVYTLPSRDELTKNOVSCLTKVKGFPSPDIAVWESNGQPE 403
Qy 418 NNYKTPPVLDSDGFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 476
Db 404 NNYKTPPVLDSDGFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 462

RESULT 12
AAW14927 standard; Protein: 470 AA.
XX
AC AAR22757;
XX
DT 20-OCT-1992 (first entry)
XX
DE Reshaped CAMPATH-1 antibody heavy chain.
XX
KW Antigen; CD8; complementarity determining region; graft rejection;
KW autoimmune diseases; rheumatoid arthritis; allergy.
XX
OS Rattus rattus.
XX
FH Key
FT Region
FT Region
FT Region
FT Region
FT Peptide
FT Peptide
FT Peptide
FT Peptide
XX WO9205274-A.
XX
XX PD 02-APR-1992.
XX
XX PP 16-SEP-1991; 91WO-GB01578.
XX
XX PR 17-SEP-1990; 90GB-0020282.
XX
XX PA (GORM/) GORMAN S D.
XX
XX PI Clark M R, Cobbold S P, Gorman S D, Waldmann H;
XX
XX DR WPI; 1992-132139/16.
XX
XX DR N-PSDB; A9233570.
XX
XX PT Humanisation of antibodies binding to human CD4 antigen - by
XX mutation of framework-encoding regions of DNA encoding variable
XX domain of rat or mouse antibody chain
XX
XX PS Disclosure; Fig 5; 74pp; English.
XX
XX PD The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.
XX

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CC Reshaped CD4 antibody can be used to induce tolerance against an
CC antigen. It can be used to alleviate autoimmune diseases such
CC as rheumatoid arthritis, and to prevent graft rejection. Tolerance
CC to a graft, e.g. an organ graft or a bone marrow transplantation can
CC also be useful to alleviate allergies. Tolerance to allergens could
CC also be achieved. See also AAR22754-R22763.
XX
SQ Sequence 470 AA;
Query Match 82.3%; Score 2122; DB 13; Length 470;
Best Local Similarity 86.6%; Pred. No. 2.1e-119;
Matches 408; Conservative 13; Mismatches 40; Indels 10; Gaps 3;
Qy 8 LLLVAAAPRWLSQVKLOOMGEGLLQPSSTLSRTCTVSGSGISGYVYWTWIRTPGRGLEW 67
Db 8 LFLVATATGVHSQVQLSESGPLVRPSQTLSTCTVSGFTFD-FYNNWVQPPGRGLEW 66
Qy 68 IGH1--YGNGATTNNPNSLKSRVTISKDTSKNOFFLNLSVTDADTAVVYCARPRDCT 125
Db 67 IGFIRDAKAGYTYEYNPSVKGRTVMTLVDTSKNQFSLSRVTAADTAVVYCARHGHTAAP 126
Qy 126 TICYGWVMDVWPGDGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTV 185
Db 127 -----FDYWGQGLVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTV 179
Qy 186 SWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKA 245
Db 180 SWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKA 239
Qy 246 PKSCDKTHTCPCPCAPPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN 305
Db 240 PKSCDKTHTCPCPCAPPELLGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN 299
Qy 306 WYVDGVEVHNKAKTPREEQNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 365
Db 300 WYVDGVEVHNKAKTPREEQNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 359
Qy 366 SKAKQPREPQVYTLPPSRDELTKNOVSCLTKVKGFPSPDIAVWESNGQPENNYKTPPP 425
Db 360 SKAKQPREPQVYTLPPSRDELTKNOVSCLTKVKGFPSPDIAVWESNGQPENNYKTPPP 419
Qy 426 VLDSGDSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 476
Db 420 VLDSGDSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 470

RESULT 13
AAW14927
ID AAW14927 standard; Protein: 467 AA.
XX
XX AC AAW14927;
XX
XX DT 18-OCT-1997 (first entry)
XX
XX DE Human gamma-4PE heavy chain.
XX
XX KW CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
XX cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
XX leukaemia; lymphoma; graft-versus-host disease; asthma;
XX transplant rejection; HIV; therapy; CE9 gamma 4PE.
XX
XX OS Homo sapiens.
XX
XX FH Key
XX FT Location/Qualifiers
XX FT Misc-difference 248 /note= "site of S229P mutation"
XX FT Misc-difference 255 /note= "site of L236E mutation"
XX
XX PN WO9709351-A1.
XX
XX PD 13-MAR-1997.
XX

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FT Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= signal\_peptide  
 FT /note= "mouse VH signal peptide sequence encoded by  
 FT synthetic linker"  
 FT Protein 20..472  
 FT /label= heavy\_chain  
 FT /note= "human gamma 1 chain constant region  
 FT and the variable region from anti-rhesus D  
 FT antibody D7C2"  
 XX  
 PN FR2724182-A1.  
 XX  
 PD 08-MAR-1996.  
 XX  
 PF 02-SEP-1994; 94FR-0010566.  
 XX  
 PR 02-SEP-1994; 94FR-0010566.  
 XX  
 PA (INSP ) INST PASTEUR.  
 PA (PROT-) PROTEINE PERFORMANCE.  
 XX  
 PI Chaabihi H, Edelman L, Kaczorek M, Margaritte C;  
 XX  
 DR WPI; 1996-162018/17.  
 XX  
 DR N-PSDB; AAT26889.  
 XX  
 PT Recombinant anti-rhesus D monoclonal antibody - expressed by  
 PT baculovirus-transformed insect cells and useful for preventing  
 PT haemolysis in new-born babies  
 XX  
 PS Example 2; Page 35-37; 46pp; French.  
 XX  
 CC The human monoclonal antibody D7C2, of isotype IgM, recognises a  
 CC 30-32 kD polypeptide on the membrane of rhesus positive red blood  
 CC cells. The antibody agglutinates rhesus positive cells but not  
 CC rhesus negative cells and is useful diagnostically and also for  
 CC preventing haemolysis in new-born rhesus positive babies.  
 CC Recombinant IGM-D7C2 can be produced by insect cells which have  
 CC been transformed by a baculoviral vector comprising a D7C2  
 CC expression cassette. The present sequence is that of a recombinant  
 CC IGM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.  
 XX  
 SQ Sequence 472 AA;  
 XX  
 Query Match 86.3%; Score 2223; DB 17; Length 472;  
 Best Local Similarity 90.6%; Pred. No. 1.9e-125;  
 Matches 425; Conservative 8; Mismatches 32; Indels 4; Gaps 3;  
 QY 8 LLLVAAPRWLSQVKLOQEGGLQPSLTSRTCVVSGSISGYYYWTWIRQTPGRGLEW 67  
 DB 8 LFLVATATGVHSQVQLQQAGLLKPSLTSCTCTVYGGSPSG-YVWSWIRQTPGRGLEW 66  
 QY 68 IGHYNGATTNNYPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYYCARGPRPDCTTI 127  
 DB 67 IGEINHSQ-STNYNPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYYCARGPRPDCTTI 123  
 QY 128 CYGGWVDVNGPDVLTVSSASTKGSVFLAPSKSSTSGGTAALGCLVKDYFPEPTVSW 187  
 DB 124 YHGDWFDPMGQGTVTTVSSASTKGSVFLAPSKSSTSGGTAALGCLVKDYFPEPTVSW 183  
 QY 188 NSGALTSGVHTTFAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKVDKKAEPK 247  
 DB 184 NSGALTSGVHTTFAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKVDKKAEPK 243  
 QY 248 SCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVFENNY 307  
 DB 244 SCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVFENNY 303  
 QY 308 VDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK 367  
 DB 304 VDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISK 363

QY 368 AKQPREPOVYTLPSRDELTKNQVSLTCLVKGPYPSDIAVEHESNGQPENNYKTTTPVL 427  
 DB 364 AKQPREPOVYTLPSRDELTKNQVSLTCLVKGPYPSDIAVEHESNGQPENNYKTTTPVL 423  
 QY 428 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476  
 DB 424 DSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 472  
 RESULT 11  
 AAB26884  
 ID AAB26884 standard; Protein; 462 AA.  
 XX  
 AC AAB26884;  
 XX  
 DT 01-FEB-2001. (first entry)  
 XX  
 DE Human immunoglobulin heavy chain amino acid sequence.  
 XX  
 KW Monoclonal antibody; immunoglobulin heavy chain; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WC200058499-A1.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 30-MAR-2000; 2000WO-JP02022.  
 XX  
 PR 30-MAR-1999; 99JP-0087929.  
 XX  
 PA (NISR ) JAPAN TOBACCO INC.  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Kusunoki C, Fukushima A;  
 XX  
 DR WPI; 2000-611721/58.  
 DR N-PSDB; AAA09695.  
 XX  
 PT Transformation of a hybridoma with a gene encoding an immunoglobulin  
 PT heavy chain polypeptide for enhanced production of monoclonal antibody  
 PT  
 XX  
 PS Example 2; Page 40-43; 48pp; Japanese.  
 XX  
 CC This invention relates to a method for the production of a monoclonal  
 CC antibody. The antibody is produced by inserting a gene encoding an  
 CC immunoglobulin heavy chain polypeptide into cells which produce a  
 CC monoclonal antibody recognizing the immunoglobulin, and culturing the  
 CC transformant to express the antibody. The invention also includes  
 CC monoclonal antibody-expressing cells transformed by the method; and  
 CC transgenic non-human animals containing the cells and expressing a human  
 CC antibody. The method results in the enhanced expression of a monoclonal  
 CC antibody for diagnostic and therapeutic use. The present sequence  
 CC represents a human immunoglobulin heavy chain amino acid sequence, the  
 CC cDNA encoding the protein is used in an example of the method of the  
 CC invention.  
 XX  
 SQ Sequence 462 AA;  
 XX  
 Query Match 82.7%; Score 2131; DB 21; Length 462;  
 Best Local Similarity 85.4%; Pred. No. 6e-120;  
 Matches 409; Conservative 18; Mismatches 32; Indels 20; Gaps 6;  
 QY 1 MKHLWFFLLVAAPRWLSQVKLOQEGGLQPSLTSRTCVVSGSISGYYYWTWIRQ 60  
 DB 1 MKHLWFFLLVAAPRWLSQVKLOQEGGLQPSLTSRTCVVSGSISGYYYWTWIRQ 59  
 QY 61 PGKLEWIGHIYNGATTNNYPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYYCARGP 120  
 DB 60 PGKLEWIGHIYNGATTNNYPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYYCAR-- 116  
 QY 121 RPCTTICVGGWV---DVWGPGLDVTVSSASTKGSVFLAPSKSSTSGGTAALGCLVKD 177

CC The present sequence is useful in the diagnosis, treatment and  
 CC prevention of disorders associated with the immune system and  
 CC cell proliferation.

XX SQ Sequence 470 AA;

Query Match 87.8%; Score 2262; DB 21; Length 470;

Best Local Similarity 90.4%; Pred. No. 8.7e-128;

Matches 433; Conservative 11; Mismatches 23; Indels 12; Gaps 5;

QY 1 MKHLWFFLLVAAPRWLSQVQLQWEGGLQPSSETLSRTCVVSGSGISGYVYTWIRQT 60  
 DB 1 MKHLWFFLLVAAPRWLSQVQLQWEGGLQPSSETLSRTCVVSGSGISGYVYTWIR 59  
 QY 61 PGRGLEWIGHYNGGATTNNYNSLKRVTISKDTSKNOFFFLNLSVTDADTAVYYCARGP 120  
 DB 60 PGRGLEWIGHYVTSYSG-STNYNSLKRVTISKDTSKNOFFFLNLSVTDADTAVYYCAR-P 117  
 QY 121 RPDCTTICYGWVDVNV---GPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKD 177  
 DB 118 PPNATT-----TTVMTSGAKGALVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKD 171  
 QY 178 YFPEPVTVSNMGALTSVGHVTPPAVLQSSGLYSLSSVTVPSSSSLGTQTYICNVNHRKPSN 237  
 DB 172 YFPEPVTVSNMGALTSVGHVTPPAVLQSSGLYSLSSVTVPSSSSLGTQTYICNVNHRKPSN 231  
 QY 238 TKVDKKAEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKOTLMISRTPEVTCVVDVSH 297  
 DB 232 TKVDKKAEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKOTLMISRTPEVTCVVDVSH 291  
 QY 298 EDEVEFNWYVDGVEVHNATKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 357  
 DB 292 EDEVEFNWYVDGVEVHNATKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 351  
 QY 358 PAPEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 417  
 DB 352 PAPEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 411  
 QY 418 NNYKTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476  
 DB 412 NNYKTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470

RESULT 9

AAAR93553  
 ID AAR93553 standard; Protein; 475 AA.

XX AC AAR93553;

XX DT 20-AUG-1996 (first entry)

XX DE Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.

XX KW Polymerase chain reaction; primer; amplify; PCR; light chain; MAB;  
 XX 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 XX FT Peptide 1..19  
 XX FT Protein /note= "Signal peptide"  
 XX FT Protein 20..475  
 XX FT Protein /note= "Mature heavy chain"

XX PN JP08038178-A.

XX PD 13-FEB-1996.

XX PF 20-FEB-1995; 95JP-0030742.

XX PR 18-FEB-1994; 94JP-0021628.

XX PA (NISN ) NISSHINO IND INC.

PA (TANA/) TANAKA H.

XX MPI; 1996-154852/16.

DR N-PSDB; AAT18059.

XX Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -  
 PT produced by primer amplification, used in the diagnosis of hCMV  
 PT infection

XX Claim 4; Page 16-18; 22pp; Japanese.

XX The sequences given in AAR93553-54 represent the heavy and light chains  
 CC respectively of a monoclonal antibody against a 65 kD antigen of human  
 CC cytomegalovirus (hCMV). The DNA s encoding these sequences were  
 CC amplified using the sequences given in AAT18040-58. The monoclonal  
 CC antibody may be used in the diagnosis of hCMV.

XX SQ Sequence 475 AA;

Query Match 86.6%; Score 2230.5; DB 17; Length 475;

Best Local Similarity 89.7%; Pred. No. 6.8e-126;

Matches 428; Conservative 11; Mismatches 35; Indels 3; Gaps 3;

QY 1 MKHLWFFLLVAAPRWLSQVQLQWEGGLQPSSETLSRTCVVSGSGISGYVYTWIRQ 59

DB 1 MKHLWFFLLVAAPRWLSQVQLQWEGGLQPSSETLSRTCVVSGSGISRSYSWGCIRQ 60

QY 60 TPGRGLEWIGHYNGGATTNNYNSLKRVTISKDTSKNOFFFLNLSVTDADTAVYYCARG 119

DB 61 PPGKLEWIGHYVTSYSG-STYNSLKRVTISKDTSKNOFFFLNLSVTDADTAVYYCAR- 118

QY 120 PRPDCTTICYGWVDVNVGPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYF 179

DB 119 TSPQYDILLTSGPSYMGQGTTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYF 178

QY 180 PEPVTVSNMGALTSVGHVTPPAVLQSSGLYSLSSVTVPSSSSLGTQTYICNVNHRKPSNTK 239

DB 179 PEPVTVSNMGALTSVGHVTPPAVLQSSGLYSLSSVTVPSSSSLGTQTYICNVNHRKPSNTK 238

QY 240 VDKKAEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKOTLMISRTPEVTCVVDVSHED 299

DB 239 VDKKVEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKOTLMISRTPEVTCVVDVSHED 298

QY 300 PSEKFNWYVDGVEVHNATKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359

DB 299 PSEKFNWYVDGVEVHNATKPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 358

QY 360 PIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419

DB 359 PIEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 418

QY 420 YKTTTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476

DB 419 YKTTTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 10

AAAR93166

ID AAR93166 standard; Protein; 472 AA.

XX AC AAR93166;

XX DT 30-OCT-1996 (first entry)

XX DE Anti-rhesus D recombinant antibody D7C2 heavy chain.

XX KW Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;  
 XX rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain;  
 XX variable region; insect host cell; baculovirus; recombinant production.

XX OS Homo sapiens.

XX OS Synthetic.



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PS Claim 1; Column 53-56; 54pp; English.
XX
CC The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ Sequence 473 AA;
Query Match 88.4%; Score 2277.5; DB 22; Length 473;
Best Local Similarity 90.8%; Pred. No. 1e-128;
Matches 434; Conservative 16; Mismatches 21; Indels 7; Gaps 4;
QY 1 MKHLFFLLVAAAPRWLSQVKLQWGGGLQPSLTSLRTCTVVGSGSI-SGYYYWTWIRQ 59
DB 1 MKHLFFLLVAAAPRWLSQVKLQWGGGLQPSLTSLRTCTVVGSGSI-SGYYYWTWIRQ 60
QY 60 TPGRLGIEWIGHYGGATNNPISLKSRTVTSKQFSLKNOFFLNLSVTDADTAVYYCARG 119
DB 61 PFGKLEWIGYIYSGSTL-INPISLKSRTVTSKQFSLKNOFFLNLSVTDADTAVYYCAR- 118
QY 120 PRPDCTTICYGW--VDVMGPGDLVTVSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDY 178
DB 119 ---DVGRLGGNYGMDVWGQGLTVTVSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDY 175
QY 179 PEPVTVSNWNSGALTSVHTPAVLQSSGLVSLSSVTVVPSSSLGTQTYICNVNHPKPSNT 238
DB 176 PEPVTVSNWNSGALTSVHTPAVLQSSGLVSLSSVTVVPSSSLGTQTYICNVNHPKPSNT 235
QY 239 KVDKAEKPKSCDKTHCTCPAPPELLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSH 298
DB 236 KVDKEVEPKSCDKTHCTCPAPPELLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSH 295
QY 299 DPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 358
DB 296 DPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 355
QY 359 APIETKISKAGQPEPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 418
DB 356 APIETKISKAGQPEPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 415
QY 419 NYKTPPVLDSDGFFLYSKLTVDKSRQQQGNVFCSCVMHEALHNNHYYTQKLSLSLSPGK 476
DB 416 NYKTPPVLDSDGFFLYSKLTVDKSRQQQGNVFCSCVMHEALHNNHYYTQKLSLSLSPGK 473
RESULT 8
AA44721
ID AAY44721 standard; Protein; 470 AA.
XX
AC AA44721;
XX
DT 25-APR-2000 (first entry)
XX
DE Human immune system molecule, ISMO-2.
XX
KW Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
KW treatment; prevention; cell proliferation; immune system disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Signal_peptide
FT Protein /label= Mature_ISMO-2
FT Modified-site 120
FT /note= "N-glycosylated"
FT Modified-site 320
FT /note= "N-glycosylated"
FT Modified-site 105
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 232
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 290
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 377
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 47
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 81
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 92
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 98
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 142
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 154
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 322
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 347
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 460
FT /note= "Protein kinase C phosphorylation site"
FT Modified-site 69
FT /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 319
FT /note= "Tyrosine kinase phosphorylation site"
FT Region 387..409
FT Region 446..463
FT Domain 34..116
FT /note= "shows similarity to Ig superfamily protein domain"
FT Domain 160..225
FT /note= "shows similarity to Ig superfamily protein domain"
FT Domain 383..450
FT /note= "shows similarity to Ig superfamily protein domain"
XX WO200000608-A2.
XX
XX 06-JAN-2000.
XX
XX 21-JUN-1999; 99WO-US13995.
XX
XX 30-JUN-1998; 98US-0107223.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Lal P, Tang YT, Corley NC, Gorgone G, Guegler KJ, Patterson C;
XX Baughn MR;
XX WPI; 2000-170916/15.
XX N-PSDB; AAZ50012.
XX
XX Immune system molecules used in the diagnosis, treatment and prevention
XX of disorders associated with the immune system and cell proliferation
XX
XX Claim 1; Pages 60-61; 69pp; English.
XX
XX The present sequence is an immune system molecule,
XX ISMO-2 from an Incyte clone 2849752 isolated from the human breast
XX tumour cDNA library (BRSTRUT13). This sequence is expressed in several
XX libraries, generally those associated with cancer, cell
XX proliferation, immune response or trauma. It shows homology to
XX vertebrate immunoglobulin gamma heavy-chain.
```

QY 361 IBKTSKAGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPENNY 420  
 Db 361 IBKTSKAGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPENNY 420  
 QY 421 KTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 476  
 Db 421 KTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 476

RESULT 6  
 AAU11646  
 ID AAU11646 standard; Protein; 476 AA.  
 XX  
 AC AAU11646;  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Protein sequence of primatised form of the heavy chain of 16C10 antibody.  
 KW Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;  
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;  
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;  
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;  
 KW graft-vs-host disease; immunosuppression; organ rejection;  
 KW interleukin-2; IL-2; mutant; mutein.  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Macaca sp.  
 OS Synthetic.  
 XX  
 PN WO200189567-A1.  
 XX  
 PD 29-NOV-2001.  
 XX  
 PF 22-MAY-2001; 2001WO-US16364.  
 XX  
 PR 22-MAY-2000; 2000US-0576424.  
 XX  
 PA (IDEC-) IDEC PHARM CORP.  
 XX  
 PI Anderson DR, Hanna N, Brame P;  
 XX  
 DR WPI; 2002-089895/12.  
 XX  
 DR N-PSDB; AAS17247.  
 XX  
 XX  
 PT Use of monoclonal antibody which specifically binds to B7.1 antigen  
 CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,  
 treating cancer, graft-vs-host disease and autoimmune disease such as  
 allergy -  
 XX  
 PS Example 8; Fig 5b; 89pp; English.  
 XX  
 CC The present invention relates to a new use of a monoclonal antibody  
 which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen  
 (CD86) for inducing the apoptosis of B7+ cells. The invention is  
 useful for treating diseases such as B cell cancer, lymphoma, a  
 cancer where B cells promote the growth and/or metastasis of tumours,  
 B cell lymphoma, B cell leukaemia, and autoimmune diseases such as  
 idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,  
 type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic  
 anaemia, inflammatory bile disease, allergy, multiple sclerosis  
 or graft-vs-host disease. The antibody is useful for immunosuppression  
 in a human or animal and for treating or preventing resistance to or  
 rejection of transplanted organ or tissue for treating proliferative  
 and hyperproliferative diseases, for treating reversible obstructive  
 airways disease, intestinal inflammations and allergies e.g. Crohn's  
 disease and ulcerative colitis, food-related allergies e.g. migraine,  
 rhinitis and eczema, and other types of allergies. The present protein  
 sequence represents the heavy chain of 16C10, a primatised antibody  
 used in the invention to induce apoptosis and inhibit production of  
 interleukin-2 (IL-2).  
 XX  
 SQ Sequence 476 AA;

Query Match 89.6%; Score 2309; DB 23; Length 476;  
 Best Local Similarity 91.2%; Pred. No. 1.4e-130;  
 Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAPRWLSQVQLQWGEGLQPSSETLSRTCTVVGSGSISGYIYWTWIRQT 60  
 Db 1 MKHLWFFLLVAAPRWLSQVQLQWGEGLQPSSETLSRTCTVVGSGSISGYIYWTWIRQT 60  
 QY 61 PORGLEWIGHYGNATNYPNPSLKSRVTISKDTSKNOFFNLNSVTDATATYVYCARGP 120  
 Db 61 PORGLEWIGHYGNATNYPNPSLKSRVTISKDTSKNOFFNLNSVTDATATYVYCARGP 120  
 QY 121 RPDCITICYGWVDWVGPDVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180  
 Db 121 LFSVVGMYNNWFDWVGPDVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180  
 QY 181 EPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKV 240  
 Db 181 EPVTVMNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKV 240  
 QY 241 DKKAEPKSCDTHTCPAPPELLGGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300  
 Db 241 DKKAEPKSCDTHTCPAPPELLGGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300  
 QY 301 EVKFNWYVDGVEVHNAKTKPREEQNTSYRVSVLTVLHQDWLNGKEYCKVSNKALPAP 360  
 Db 301 EVKFNWYVDGVEVHNAKTKPREEQNTSYRVSVLTVLHQDWLNGKEYCKVSNKALPAP 360  
 QY 361 IEKTSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPENNY 420  
 Db 361 IEKTSKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPENNY 420  
 QY 421 KTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 476  
 Db 421 KTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 476

RESULT 7  
 AAB36206  
 ID AAB36206 standard; protein; 473 AA.  
 XX  
 AC AAB36206;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Human immune system associated protein HisAP-4.  
 XX  
 KW Human; immune system associated protein; HisAP-4; immune disorder;  
 infection; autoimmune disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6135941-A.  
 XX  
 PD 24-OCT-2000.  
 XX  
 PF 27-MAR-1998; 98US-0049672.  
 XX  
 PR 27-MAR-1998; 98US-0049672.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;  
 Hillman J, Au-Young J;  
 XX  
 WPI; 2001-030926/04.  
 DR N-PSDB; AAC66522.  
 DR  
 PT New human immune system associated proteins (HisAP) and polynucleotides  
 encoding the HisAP, useful for diagnosing, treating or preventing  
 immune or cell proliferative disorders or infections -  
 XX

```
XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
XX
XX Claim 14; Fig 10B; 8lpp; English.
XX
CC 2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human
CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
CC heavy variable genes (see also AAT62512 and AAT62513) are inserted into
CC an expression vector (pref. NEOSPPLA) which contains human light and
CC heavy chain constant genes to allow prodn. of the primatised
CC antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC antibodies have also been produced (see also AAW01817-20). The
CC primatised antibodies inhibit the B7:CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders
CC and graft-versus-host disease.
XX
XX Sequence 476 AA;
Query Match 89.6%; Score 2309; DB 18; Length 476;
Best Local Similarity 91.2%; Pred. No. 1.4e-130;
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;
QY 1 MKHLWFFLLVAAPRWLSQVQLQWGGELLPQSETLSRTCTVSGSGISGYVYWTWIRQT 60
DB 1 MKHLWFFLLVAAPRWLSQVQLQWGGELLPQSETLSLTCAVSGSGISGYGWMIRQP 60
QY 61 PGRGLEWIGHYNGATTNYPNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYYCARGP 120
DB 61 PGRGLEWIGSFYSSGNTYYPNPSLKSVQTIISTDTSKNQFSLKLSMTAADTAVYYCVRDR 120
QY 121 RPDCTTICVGGWVDVWGPDLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYEP 180
DB 121 LFSVGVGVYNNWDFVWGPGLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFP 180
QY 181 EPVTVSNWNSGALTSQVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQYICNVNHPKSNTKV 240
DB 181 EPVTVSNWNSGALTSQVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQYICNVNHPKSNTKV 240
QY 241 DKAEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKAEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
QY 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTIKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
QY 421 KTTTPVLSDSGSFFLYSKLTVDKSRWQQGNVPCSWMEALHNNHYTQKLSLSPGK 476
DB 421 KTTTPVLSDSGSFFLYSKLTVDKSRWQQGNVPCSWMEALHNNHYTQKLSLSPGK 476
RESULT 5
AAW63765
ID AAW63765 standard; Protein; 476 AA.
XX
XX AAW63765;
XX
DT 29-SEP-1998 (first entry)
DE
DE Macaque primatised 16C10 heavy chain protein.
XX
XX Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
XX CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
XX T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
XX immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
XX T cell proliferation.
```

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OS Macaca fascicularis.
XX
XX WO9819706-A1.
XX
XX 14-MAY-1998.
XX
XX 29-OCT-1997; 97WO-US19906.
XX
XX 08-NOV-1996; 96US-0746361.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Anderson DR, Brams P, Hanna N;
DR WPI; 1998-286601/25.
DR N-PSDB; AAV35489.
XX
XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
XX inhibiting binding to CD28 - useful as specific immunosuppressants
XX for treating diseases that involve interactions between T and B
XX cells, e.g. graft rejection or tumours
XX
XX Example 7; Fig 5b; 87pp; English.
XX
CC This sequence represents a primatised form of the antibody 16C10 heavy
CC chain from macaque. This sequence is used in a method which studies new
CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC Mab's are specific immunosuppressants for treatment of diseases involving
CC T cell/B cell interactions, particularly autoimmune disease, specifically
CC idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC host diseases, B cell lymphoma, infections (including by human immune
CC deficiency virus) or inflammatory disease and tumours. Optionally the
CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
CC also be used as imaging agents and as vaccines or immunogens to develop
CC anti-idiotype reagents. Mab's are optionally combined with other proteins
CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC production of interleukin-2 (IL-2), T cell proliferation and
CC antigen-specific immunoglobulin G (IgG) responses.
XX
XX Sequence 476 AA;
Query Match 89.6%; Score 2309; DB 19; Length 476;
Best Local Similarity 91.2%; Pred. No. 1.4e-130;
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;
QY 1 MKHLWFFLLVAAPRWLSQVQLQWGGELLPQSETLSRTCTVSGSGISGYVYWTWIRQT 60
DB 1 MKHLWFFLLVAAPRWLSQVQLQWGGELLPQSETLSLTCAVSGSGISGYGWMIRQP 60
QY 61 PGRGLEWIGHYNGATTNYPNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYYCARGP 120
DB 61 PGRGLEWIGSFYSSGNTYYPNPSLKSVQTIISTDTSKNQFSLKLSMTAADTAVYYCVRDR 120
QY 121 RPDCTTICVGGWVDVWGPDLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFP 180
DB 121 LFSVGVGVYNNWDFVWGPGLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFP 180
QY 181 EPVTVSNWNSGALTSQVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQYICNVNHPKSNTKV 240
DB 181 EPVTVSNWNSGALTSQVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQYICNVNHPKSNTKV 240
QY 241 DKAEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKAEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTRVVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
```

QY 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420  
 DB 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420  
 QY 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK 476  
 DB 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK 476

RESULT 3  
 AAU11539  
 ID AAU11539 standard; Protein; 476 AA.  
 XX  
 AC AAU11539;  
 XX  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Protein sequence of primatised form of the heavy chain of 7C10 antibody.  
 XX  
 KW Human, macaque monkey; light chain; primatised antibody; 7C10 antibody;  
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;  
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;  
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;  
 KW graft-vs-host disease; immunosuppression; organ rejection;  
 KW interleukin-2; IL-2; mutant; mutein.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Macaca sp.  
 OS Synthetic.  
 XX  
 PN W0200189567-A1.  
 XX  
 XX  
 PD 29-NOV-2001.  
 XX  
 PF 22-MAY-2001; 2001WO-US16364.  
 XX  
 PR 22-MAY-2000; 2000US-0576424.  
 XX  
 XX (IDEC-) IDEC PHARM CORP.  
 XX  
 XX Anderson DR, Hanna N, Brama P;  
 XX  
 DR WPI; 2002-089895/12.  
 DR N-PSDB; AAS17243.  
 XX  
 XX Use of monoclonal antibody which specifically binds to B7.1 antigen  
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, as  
 PT treating cancer, graft-vs-host disease and autoimmune disease such as  
 PT allergy -  
 XX  
 PS Example 8; Fig 3b; 89pp; English.  
 XX  
 CC The present invention relates to a new use of a monoclonal antibody  
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen  
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is  
 CC useful for treating diseases such as B cell cancer, lymphoma, a  
 CC cancer where B cells promote the growth and/or metastasis of tumours,  
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as  
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosis,  
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic  
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis  
 CC or graft-vs-host disease. The antibody is useful for immunosuppression  
 CC in a human or animal and for treating or preventing resistance to or  
 CC rejection of transplanted organ or tissue for treating proliferative  
 CC and hyperproliferative diseases, for treating reversible obstructive  
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's  
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,  
 CC rhinitis and eczema, and other types of allergies. The present protein  
 CC sequence represents the heavy chain of 7C10, a primatised antibody  
 CC used in the invention to induce apoptosis and inhibit production of  
 CC interleukin-2 (IL-2).

SQ Sequence 476 AA;  
 Query Match 100.0%; Score 2577; DB 23; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-146;  
 Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKHLWFFLLVAAPRWLSQVKLQWGEGLLPSETLSRTCTCVSGSGISGYYWTWIRQT 60  
 DB 1 MKHLWFFLLVAAPRWLSQVKLQWGEGLLPSETLSRTCTCVSGSGISGYYWTWIRQT 60  
 QY 61 PGRGLEWIGHIYNGATTNYPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVYTCARGP 120  
 DB 61 PGRGLEWIGHIYNGATTNYPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVYTCARGP 120  
 QY 121 RPDCTTICVGGWVDVWPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180  
 DB 121 RPDCTTICVGGWVDVWPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180  
 QY 181 EPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHPSTNTKV 240  
 DB 181 EPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHPSTNTKV 240  
 QY 241 DKKAEPKCDKTHTCPCPAPPELLGPGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDP 300  
 DB 241 DKKAEPKCDKTHTCPCPAPPELLGPGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDP 300  
 QY 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAP 360  
 DB 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAP 360  
 QY 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420  
 DB 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420  
 QY 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK 476  
 DB 421 KTTTPVLDSGSGFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSPGK 476

## RESULT 4

AAW01822  
 ID AAW01822 standard; Protein; 476 AA.  
 XX  
 AC AAW01822;  
 XX  
 XX  
 DT 25-MAY-1997 (first entry)  
 XX  
 DE Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.  
 XX  
 KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;  
 KW primatised antibody; B7 antigen; CD28; immunosuppressive;  
 KW autoimmune disease; idiopathic thrombocytopenia purpura;  
 KW systemic lupus erythematosis; rheumatoid arthritis; psoriasis;  
 KW type 1 diabetes mellitus; graft versus host disease;  
 KW hetero-hybridoma; transfectoma.  
 XX  
 OS Chimeric Macaca cynomolgus;  
 OS Chimeric Homo sapiens.  
 XX  
 PN W09640878-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US10053.  
 XX  
 PR 07-JUN-1995; 95US-0487550.  
 XX  
 PA (IDEC-) IDEC PHARM CORP.  
 XX  
 PI Anderson DR, Brama P, Hanna N, Shestowsky WS;  
 XX  
 DR WPI; 1997-108638/10.  
 DR N-PSDB; AAT62513.

DR N-PSDB; AAT62510.  
XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -  
PT useful for treating autoimmune disease or graft-versus-host disease  
XX  
PS Claim 6; Fig 8B; 81pp; English.  
XX  
CC 2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised  
CC forms of the light and heavy chains of cynomolgus monkey anti-human  
CC B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy  
CC variable genes (see also AAT62509 and AAT62510) are inserted into  
CC an expression vector (pref. NEOSPLA) which contains human light and  
CC heavy chain constant region genes to allow prodn. of the primatised  
CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1  
CC antibodies have also been produced (see also AAW01819-22). The  
CC primatised antibodies inhibit the B7/CD28 pathway, making them  
CC useful immunosuppressants for the treatment of autoimmune disorders  
CC and graft-versus-host disease.  
XX  
SQ Sequence 476 AA;  
  
Query Match 100.0%; Score 2577; DB 18; Length 476;  
Best Local Similarity 100.0%; Pred. No. 1.2e-146;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 MKHLWFFLLVAAAPRWLSQVKLQOMGEGLLQPSLRTSCVVGSGISGYVYWTWIRQT 60  
  
Qy 61 PGRLEWIGHYGNAGTNNPNSLKSRVTISKDTSKNQFFLNLSVTDADTAVYVCARGP 120  
Db 61 PGRLEWIGHYGNAGTNNPNSLKSRVTISKDTSKNQFFLNLSVTDADTAVYVCARGP 120  
  
Qy 121 RPDCTTTCYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKTSCTGTAALGCLVKDYFP 180  
Db 121 RPDCTTTCYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKTSCTGTAALGCLVKDYFP 180  
  
Qy 181 EPTVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNK 240  
Db 181 EPTVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNK 240  
  
Qy 241 DKAEPPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDP 300  
Db 241 DKAEPPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDP 300  
  
Qy 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360  
Db 301 EVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360  
  
Qy 361 IEKTSKAGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420  
Db 361 IEKTSKAGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420  
  
Qy 421 KTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 476  
Db 421 KTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 476  
  
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AAW63761  
ID AAW63761 standard; Protein; 476 AA.  
XX  
AC AAW63761;  
XX  
XX 29-SEP-1998 (first entry)  
XX  
XX Macaque primatised 7C10 heavy chain DNA.  
XX  
KW Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;  
KW CD86; Inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;  
KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;  
KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;  
KW T cell proliferation; ss.

XX OS Macaca fascicularis.  
XX WO9819706-A1.  
XX 14-MAY-1998.  
XX  
XX 29-OCT-1997; 97WO-US19906.  
XX  
XX 08-NOV-1996; 96US-0746361.  
XX  
XX (IDEC-) IDEC PHARM CORP.  
XX  
XX Anderson DR, Brame P, Hanna N;  
XX WPI; 1998-286601/25.  
XX N-PSDB; AAV35485.  
XX  
XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and  
XX inhibiting binding to CD28 - useful as specific immunosuppressants  
XX for treating diseases that involve interactions between T and B  
XX cells, e.g. graft rejection or tumours  
XX  
XX Example 7; Fig 3b; 87pp; English.  
XX  
CC This sequence represents a primatised form of the antibody 7C10 heavy  
CC chain from macaque. This sequence is used in a method which studies new  
CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to  
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such  
CC Mab's are specific immunosuppressants for treatment of diseases involving  
CC T cell/B cell interactions, particularly autoimmune disease, specifically  
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type  
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,  
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.  
CC host diseases, B cell lymphoma, infections (including by human immune  
CC deficiency virus) or inflammatory disease and tumours. Optionally the  
CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can  
CC also be used as imaging agents and as vaccines or immunogens to develop  
CC anti-idiotypic reagents. Mab's are optionally combined with other proteins  
CC or small molecule immunosuppressants. Blocking B7/CD28 interactions  
CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits  
CC production of interleukin-2 (IL-2), T cell proliferation and  
CC antigen-specific immunoglobulin G (IgG) responses.  
XX  
SQ Sequence 476 AA;  
  
Query Match 100.0%; Score 2577; DB 19; Length 476;  
Best Local Similarity 100.0%; Pred. No. 1.2e-146;  
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 61 PGRLEWIGHYGNAGTNNPNSLKSRVTISKDTSKNQFFLNLSVTDADTAVYVCARGP 120  
  
Qy 121 RPDCTTTCYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKTSCTGTAALGCLVKDYFP 180  
Db 121 RPDCTTTCYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKTSCTGTAALGCLVKDYFP 180  
  
Qy 181 EPTVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNK 240  
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GenCore version 5.1.4\_p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 48.9575 Seconds  
(without alignments)  
1295.559 Million cell updates/sec

Title: US-09-758-173-4

Perfect score: 2577

Sequence: 1 MKHLWFFLLVAAPRWLSQ.....MHEALHHYTKSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2577	100.0	476	18 AAW01818	Primates anti-hu
2	2577	100.0	476	19 AAW63761	Macaque primatized
3	2577	100.0	476	23 AAU11539	Protein sequence o
4	2309	89.6	476	18 AAW01822	Primates anti-hu
5	2309	89.6	476	19 AAW63765	Macaque primatized
6	2309	89.6	476	23 AAU11646	Protein sequence o
7	2277.5	88.4	473	22 AAB36206	Human immune syste
8	2262	87.8	470	21 AAY44721	Human immune syste
9	2230.5	86.6	475	17 AAR93553	Monoclonal antibod
10	2223	86.3	472	17 AAR93166	Anti-rhesus D reco

11	2131	82.7	21	AAB26884	Human immunoglobul
12	2132	82.3	470	13 AAR22757	Reshaped CAMPATH-1
13	2112.5	82.0	467	18 AAW14927	Human gamma-4E he
14	2111.5	81.9	467	18 AAW14925	Human gamma-4 heav
15	2107.5	81.8	475	22 AAG63640	Amino acid sequenc
16	2104.5	81.7	467	18 AAW14926	Human gamma-4E hea
17	2104.5	81.7	581	22 AAB81972	Reshaped CD2 ep
18	2103.5	81.6	467	13 AAR22759	Reshaped CD4 antib
19	2100.5	81.5	467	13 AAR22758	Reshaped CD4 antib
20	2100	81.5	451	20 AAW95659	Mus musculus anti-
21	2100	81.5	451	20 AAW95661	Mus musculus anti-
22	2100	81.5	451	21 AAY85201	Light chain amino
23	2100	81.5	451	22 AAB74088	Anti-IgE antibody,
24	2100	81.5	451	22 AAB76948	Full length heavy,
25	2100	81.5	451	22 AAB76950	Full length heavy,
26	2092	81.2	451	20 AAY50031	Human E27 anti-IgE
27	2092	81.2	451	20 AAW95663	Mus musculus anti-
28	2092	81.2	451	21 AAB07473	Amino acid sequenc
29	2092	81.2	451	22 AAB74212	E27 anti-IgE antib
30	2092	81.2	451	22 AAB76952	Full length heavy
31	2091.5	81.2	446	17 AAW05829	Humanised 1D10 ant
32	2079.5	80.7	475	18 AAW11639	Human anti-RSV mon
33	2077	80.6	470	21 AAU77289	Protein #2 in inve
34	2073	80.4	478	19 AAW63763	Macaque primatized
35	2073	80.4	478	23 AAU11644	Protein sequence o
36	2069.5	80.3	481	13 AAR24442	Sequence of antibo
37	2069	80.3	453	14 AAR33311	Humanised MaEl1 Ve
38	2069	80.3	453	21 AAY85199	Heavy chain amino
39	2067	80.2	478	18 AAW01820	Primates anti-hu
40	2061.5	80.0	452	20 AAY29458	Recombinant immuno
41	2061.5	80.0	452	21 AAB30322	Humanised anti-IL-
42	2061.5	80.0	452	21 AAY77766	Humanised anti-IL-
43	2057.5	79.8	477	22 AAU14288	Human novel protei
44	2057	79.8	476	22 AAB49243	Chimeric 4H6 anti-
45	2053	79.7	470	21 AAB08026	A dimeric anti-CD2

#### ALIGNMENTS

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RESULT 1
AAW01818
ID AAW01818 standard; Protein; 476 AA.
AC AAW01818;
XX
XX
XX
DT 25-MAY-1997 (first entry)
DE Primatised anti-human B7.1 antigen antibody 7C10 heavy chain.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
FN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PP 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX WPI; 1997-108638/10.

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Qy	20	QVKLOQWEGELLQPSSETLSRTCVVSGSGSISGYVYWTWIRQTPGRGLEWIGHIYNGATTN	79
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Qy	80	YNPSLKSRVTISKDTSKNQFFLNLSNVDADTAVYVCARGPRPDCTTICYGGM-VDVWGP	138
Db	60	YADSVKGRFTISRDDSKNTFYLQMNSLRADTAVYVCARGSH-----YFGHWHFAVWQG	113
Qy	139	GDLVTVSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSGV	196
Db	114	GTLLTVSSASTKGKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSGV	173
Qy	197	HTFPVAVLSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKAEPKSCDKTHTCP	256
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Qy	257	PCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNA	316
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Qy	317	KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQ	376
Db	294	KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQ	353
Qy	377	VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPTPLDSDGSPFLY	436
Db	354	VYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPTPLDSDGSPFLY	413
Qy	437	SKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPGK	476
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SEQUENCE CHARACTERISTICS:  
LENGTH: 478 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-948-429B-8

Query Match 80.4%; Score 2073; DB 9; Length 478;  
Best Local Similarity 83.9%; Pred. No. 1.7e-106;  
Matches 396; Conservative 21; Mismatches 51; Indels 4; Gaps 3;

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DB 67 VGFIRKPNKGTTTEYAAVSKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYYCTTSVISHCR 126  
QY 126 -TICYGWDVVMGPGDLVTVSSASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVT 184  
DB 127 GVCYGGYEFWQGGALVTVSSASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVT 186  
QY 185 VSNWNSGALTSVHTTPAVLQSSGLSLSVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKKA 244  
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QY 245 EPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 304  
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QY 425 PVLDSDGSGFFLYSKLTVDKSRWQOGNPFVSCSVMEALHNHYTQKSLSLSPGK 476  
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RESULT 14  
US-09-925-179-8  
; Sequence 8, Application US/09925179  
; Publication No. US20030044858A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Anti-IGE Antibodies (as amended)  
; FILE REFERENCE: P07182C1C1US  
; CURRENT APPLICATION NUMBER: US/09/925,179  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 08/466,163  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 68  
; SEQ ID NO 8  
; LENGTH: 453  
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; ORGANISM: Artificial sequence  
; FEATURE:

; OTHER INFORMATION: humanized maell, version 1 heavy chain  
US-09-925-179-8

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Best Local Similarity 85.7%; Pred. No. 2.6e-106;  
Matches 394; Conservative 19; Mismatches 37; Indels 10; Gaps 4;

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RESULT 15  
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; Sequence 8, Application US/09802077  
; Patent No. US20010033842A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
; FILE REFERENCE: P07182C2US  
; CURRENT APPLICATION NUMBER: US/09/802,077  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
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; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:

; OTHER INFORMATION: humanized maell, version 1 heavy chain  
US-09-802-077-8

Query Match 80.3%; Score 2069; DB 10; Length 453;  
Best Local Similarity 85.7%; Pred. No. 2.6e-106;  
Matches 394; Conservative 19; Mismatches 37; Indels 10; Gaps 4;

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DB 186 WNSGALTSVHTFPVAVLQSSGLYSLSVVVTPSSISGTTQTYICNVNHHKPSNTKVDKKAEP 245  
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RESULT 12  
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; Sequence 8, Application US/10124905  
; Patent No. US20020166136A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/124,905  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/383,916  
; FILING DATE:  
; APPLICATION NUMBER: US 08/487,550  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 478 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-10-124-905-8

Query Match 80.4%; Score 2073; DB 9; Length 478;  
Best Local Similarity 83.9%; Pred. No. 1.7e-106;  
Matches 396; Conservative 21; Mismatches 51; Indels 4; Gaps 3;

QY 8 LLLVAAPRWVLSOVKIQWGEGLLPSETLSRTCTVVGSGISGYYTWTWIRQTTPGRGLEW 67  
DB 8 LFLVAVATRVQCEVQLVVEGGLVQPGSLRVSCAVSGFTFSDHNYM-WFRQAPGKPEW 66  
QY 68 IGHYIG--NGATTNYPNLSKSRVTISKDTSKNOFFFLNLSVTDADTAVVYCARGRPDPCT 125  
DB 67 VGFIRKPNNGTTEYAAASVADRFITSRDDSKSIAYLQMSLSKIEDTAVVYCTTSYISHCR 126  
QY 126 -TTCYCGWVDVWPGDLVTVSSASTKPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVT 184  
DB 127 GVCYGGYFEGWQAGALVTVSSASTKPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVT 186  
QY 185 VSNWNGALTSVHTFPVAVLQSSGLYSLSVVVTPSSISGTTQTYICNVNHHKPSNTKVDKKA 244  
DB 187 VSNWNGALTSVHTFPVAVLQSSGLYSLSVVVTPSSISGTTQTYICNVNHHKPSNTKVDKKA 246  
QY 245 EPKSCDKHTHTCPCPAPELLGSPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKF 304  
DB 247 EPKSCDKHTHTCPCPAPELLGSPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKF 306  
QY 305 NWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 364  
DB 307 NWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 366  
QY 365 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 424  
DB 367 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 426  
QY 425 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 476  
DB 427 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 478

RESULT 13  
US-09-948-429B-8  
; Sequence 8, Application US/09948429B  
; Patent No. US20020177689A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/948,429B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/383,916  
; FILING DATE:  
; APPLICATION NUMBER: US 08/487,550  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 8:

;  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table  
US-09-925-179-68

Query Match 81.5%; Score 2099; DB 9; Length 451;  
Best Local Similarity 86.7%; Pred. No. 6e-108;  
Matches 397; Conservative 18; Mismatches 35; Indels 8; Gaps 3;

QY 20 QVKLQWGGELGLOPSTLRTCTVVGSGISGYYYWTWIRQTGRLGIEWIGHIYNGATTN 79  
Db 1 EVQLVESGGGLVPGGSLRLSCAAGVSIITSGYSMWIRQAPGKGLIEWASIKYSG-ETK 59  
QY 80 YNPSLKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTTICYGGM-VDVWGP 138  
Db 60 YNPVSKGRITISRDDSKNTFYQLQNSRAEDTAVYVCARGSH-----YFGHWHFAVMGQ 113  
QY 139 GDLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHT 198  
Db 114 GTLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHT 173  
QY 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEKPKSCDKTHTCPPC 258  
Db 174 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEKPKSCDKTHTCPPC 233  
QY 259 PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318  
Db 234 PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293  
QY 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378  
Db 294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353  
QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 438  
Db 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 413  
QY 439 LTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 476  
Db 414 LTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 451

RESULT 10  
US-09-920-171-18  
; Sequence 18, Application US/09920171  
; Patent No. US20020054878A1  
; GENERAL INFORMATION:  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Lowe, John  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)  
; FILE REFERENCE: P1123C2US  
; CURRENT APPLICATION NUMBER: US/09/920,171  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: US 08/887,352  
; PRIOR FILING DATE: 1997-07-02  
; PRIOR APPLICATION NUMBER: US 09/296,005  
; PRIOR FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 18  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-920-171-18

Query Match 81.2%; Score 2092; DB 10; Length 451;  
Best Local Similarity 86.2%; Pred. No. 1.4e-107;  
Matches 395; Conservative 19; Mismatches 36; Indels 8; Gaps 3;

QY 20 QVKLQWGGELGLOPSETLSRTCTVVGSGISGYYYWTWIRQTGRLGIEWIGHIYNGATTN 79  
Db 1 EVQLVESGGGLVPGGSLRLSCAAGVSIITSGYSMWIRQAPGKGLIEWASIKYSG-ETK 59  
QY 80 YNPSLKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTTICYGGM-VDVWGP 138  
Db 60 YNPVSKGRITISRDDSKNTFYQLQNSRAEDTAVYVCARGSH-----YFGHWHFAVMGQ 113  
QY 139 GDLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHT 198  
Db 114 GTLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHT 173  
QY 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEKPKSCDKTHTCPPC 258  
Db 174 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKAEKPKSCDKTHTCPPC 233  
QY 259 PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318  
Db 234 PAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293  
QY 319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378  
Db 294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353  
QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 438  
Db 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSK 413  
QY 439 LTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 476  
Db 414 LTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 451

RESULT 11  
US-09-740-002-25  
; Sequence 25, Application US/09740002  
; Patent No. US20020001798A1  
; GENERAL INFORMATION:  
; APPLICANT: BRAMS, PETER  
; APPLICANT: MORROW, PHILLIP  
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR  
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF  
; FILE REFERENCE: 037003-0275759  
; CURRENT APPLICATION NUMBER: US/09/740,002  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 09/335,697  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 08/488,376  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-740-002-25

Query Match 80.5%; Score 2075.5; DB 10; Length 475;  
Best Local Similarity 84.9%; Pred. No. 1.2e-106;  
Matches 399; Conservative 25; Mismatches 43; Indels 3; Gaps 3;

QY 8 LLLVAAPRWLSQVKLOOWGEGLLQPSSETLSRTCTVVGSGISGYYYW-TWIRQTGRLGLE 66  
Db 8 LFLVAVATRWLSQVKLOOWGEGLLQPSSETLSRTCTVVGSGISGYYYW-TWIRQTGRLGLE 67  
QY 67 WIGHIYNGATTNYPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTT 126  
Db 68 WLGNIFFSSD-EKSFSPSLKSRLTTSQDTSRSQVLSLTNVDPVDTATYICARVGLDYNA 126  
QY 127 ICYGGWVDVWGPGLDVTVSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVS 186  
Db 127 Y-YLYLDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVS 185

```
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match      81.5%; Score 2100; DB 10; Length 451;
Best Local Similarity 86.5%; Pred. No. 5.3e-108;
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

QY 20 QVKLQWGEGLLPSETLSRTCVVSGSISGYIYWTWIRQTPGRGLEWIGHIYNGATTN 79
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDG-STN 59
QY 80 YNPSLKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTTICYGGW-VDVWGP 138
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYVCARGSH-----YFGHWHFAVWGP 113
QY 139 GDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHT 198
Db 114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHT 173
QY 199 FPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKAEKPSCKDTHTCPPC 258
Db 174 FPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKAEKPSCKDTHTCPPC 233
QY 259 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db 234 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 378
Db 294 KPREEQYNSTYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 353
QY 379 TLPSPRDELTKQVSLTCLVKGYFSPDIAVEVESNGQPNENYKTTTPPVLDSGSPFLYSK 438
Db 354 TLPSPREEMTKQVSLTCLVKGYFSPDIAVEVESNGQPNENYKTTTPPVLDSGSPFLYSK 413
QY 439 LTVDKSRWQGGNVFSCVMHEALHNHYTQKSLSLSPGK 476
Db 414 LTVDKSRWQGGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 8
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
```

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; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

Query Match      81.5%; Score 2100; DB 10; Length 451;
Best Local Similarity 86.5%; Pred. No. 5.3e-108;
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

QY 20 QVKLQWGEGLLPSETLSRTCVVSGSISGYIYWTWIRQTPGRGLEWIGHIYNGATTN 79
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDG-STN 59
QY 80 YNPSLKSRVTISKDTSKNOFFLNLSVTDADTAVYVCARGPRDCTTICYGGW-VDVWGP 138
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYVCARGSH-----YFGHWHFAVWGP 113
QY 139 GDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHT 198
Db 114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHT 173
QY 199 FPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKAEKPSCKDTHTCPPC 258
Db 174 FPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKAEKPSCKDTHTCPPC 233
QY 259 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
Db 234 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293
QY 319 KPREEQYNSTYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 378
Db 294 KPREEQYNSTYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 353
QY 379 TLPSPRDELTKQVSLTCLVKGYFSPDIAVEVESNGQPNENYKTTTPPVLDSGSPFLYSK 438
Db 354 TLPSPREEMTKQVSLTCLVKGYFSPDIAVEVESNGQPNENYKTTTPPVLDSGSPFLYSK 413
QY 439 LTVDKSRWQGGNVFSCVMHEALHNHYTQKSLSLSPGK 476
Db 414 LTVDKSRWQGGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 9
US-09-925-179-68
; Sequence 68, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 68
; LENGTH: 451
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## RESULT 5

```

US-09-925-179-66
; Sequence 66, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IGE Antibodies (a
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: FCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 66
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain
US-09-925-179-66

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Query Match	81.6%	Score 2103	DB 9	Length 451
Best Local Similarity	86.7%	Pred. No. 3.6e-108		
Matches 397	Conservative	19	Mismatches 34	Indels 8
			Gaps 3	

```

; Sequence 65, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Paula M.
; APPLICANT: Jardieu, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925.179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-25
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8b of Table
US-09-925-179-65

Query Match      81.5%; Score 2100; DB 9; Length 451;
Best Local Similarity 86.5%; Pred. No. 5.3e-108;
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

```

Qy	20	QYKLOOMGEGLOPSETLSR	TCVSGGSI	SGYYWTW	IRQTPGRGLEWIGHIYNGATTN	79				
Db	1	EVLVESGGGLVQPGGSLRL	SCAVSGY	SITSGYSWN	IRQAPGKGLEWASITYDG-STN	59				
Qy	80	YNPSLKS	RVTISK	DTSKNO	FFLNLSVDTADATANY	YCARGRPDCITICYGGH-VDVWCP	138			
Db	60	YNPSVKG	RIITIS	RDDSKNTY	QOMNSLRAEDTAV	YCARGSH-----YFGWHFVAWQ	113			
Qy	139	GDLVTV	SASTK	GPSVF	PLAPSSK	TSGGTAALGCLVKDYFPEPVTVMNSGALTSVGH	198			
Db	114	GTLVTV	SASTK	GPSVF	PLAPSSK	TSGGTAALGCLVKDYFPEPVTVMNSGALTSVGH	173			
Qy	199	PAVLQ	SGSLY	SLSSVV	TVPPSS	SLGTQYICNVNHNKPSNTKYDKAEPKSCDKTHTCP	258			
Db	174	PAVLQ	SGSLY	SLSSVV	TVPPSS	SLGTQYICNVNHNKPSNTKYDKAEPKSCDKTHTCP	233			
Qy	259	PAPELL	GGPSV	FLFP	PKPKD	TLMI	SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAT	318		
Db	234	PAPELL	GGPSV	FLFP	PKPKD	TLMI	SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAT	293		
Qy	319	KPREEQ	YNSTYR	VVSV	LVTLV	HDWLNGEYKCKVSNKALPAPI	EKTISKA	KGPREPQY	378	
Db	294	KPREEQ	YNSTYR	VVSV	LVTLV	HDWLNGEYKCKVSNKALPAPI	EKTISKA	KGPREPQY	353	
Qy	379	TLPPSR	DELTK	NOVSL	TCLVK	GPSPDIA	VEWESNGQPENNYK	TTTPVLDS	DCSGFP	438
Db	354	TLPPSR	DEMTK	NOVSL	TCLVK	GPSPDIA	VEWESNGQPENNYK	TTTPVLDS	DCSGFP	413
Qy	439	LTVDKSR	WQGNV	FCSCV	MHEAL	LHNHY	TQKSL	SLSPGK	476	
Db	414	LTVDKSR	WQGNV	FCSCV	MHEAL	LHNHY	TQKSL	SLSPGK	451	

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICANT: Anderson, Darrell R.  
FILING DATE: 07-JUN-1995  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-10-124-905-12

Query Match 89.6%; Score 2309; DB 9; Length 476;  
Best Local Similarity 91.2%; Pred. No. 2.1e-119;  
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKHLWFLLLVAAPRWLSQVQLQWGGELGLQPSSETLSRVCVWSGGISGGYVYWTWIRQT 60  
DB 1 MKHLWFLLLVAAPRWLSQVQLQWGGELGLQPSSETLSRVCVWSGGISGGYVYWTWIRQT 60  
QY 61 PGKLEWIGHIYNGCATNNYNPSLKSRTISKDTSKQFSLKLSMTAADAATVYVCVRDR 120  
DB 61 PGKLEWIGHIYNGCATNNYNPSLKSRTISKDTSKQFSLKLSMTAADAATVYVCVRDR 120  
QY 121 RPDCTTICGGWVDVWVGPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGLVKDYFP 180  
DB 121 RPDCTTICGGWVDVWVGPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGLVKDYFP 180  
QY 181 EPTVSNWNGALTSQVHFPFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKV 240  
DB 181 EPTVSNWNGALTSQVHFPFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKV 240  
QY 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300  
DB 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300  
QY 301 EVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360  
DB 301 EVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360  
QY 361 IEKTSKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNY 420  
DB 361 IEKTSKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNY 420  
QY 421 KTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476  
DB 421 KTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 4  
US-09-948-429B-12  
Sequence 12, Application US/09948429B  
Patent No. US20020177689A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 07-JUN-1995  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-948-429B-12

Query Match 89.6%; Score 2309; DB 9; Length 476;  
Best Local Similarity 91.2%; Pred. No. 2.1e-119;  
Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 1 MKHLWFLLLVAAPRWLSQVQLQWGGELGLQPSSETLSRVCVWSGGISGGYVYWTWIRQT 60  
DB 1 MKHLWFLLLVAAPRWLSQVQLQWGGELGLQPSSETLSRVCVWSGGISGGYVYWTWIRQT 60  
QY 61 PGKLEWIGHIYNGCATNNYNPSLKSRTISKDTSKQFSLKLSMTAADAATVYVCVRDR 120  
DB 61 PGKLEWIGHIYNGCATNNYNPSLKSRTISKDTSKQFSLKLSMTAADAATVYVCVRDR 120  
QY 121 RPDCTTICGGWVDVWVGPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGLVKDYFP 180  
DB 121 RPDCTTICGGWVDVWVGPGDLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGLVKDYFP 180  
QY 181 EPTVSNWNGALTSQVHFPFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKV 240  
DB 181 EPTVSNWNGALTSQVHFPFPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKV 240  
QY 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300  
DB 241 DKAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP 300  
QY 301 EVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360  
DB 301 EVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360  
QY 361 IEKTSKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNY 420  
DB 361 IEKTSKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNY 420  
QY 421 KTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476  
DB 421 KTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-4

Query Match      100.0%; Score 2577; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.6e-134;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKHLWFFLLVAAPRWLSQVKLQWEGGLQPSSETLSRTCVVSGSISGYIYWTWIRQT 60
QY 61 PGRGLEWIGHIYGNAGATTNPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVVYCARGP 120
DB 61 PGRGLEWIGHIYGNAGATTNPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVVYCARGP 120
QY 121 RPDCTTICYGWVDVWVGPDGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
DB 121 RPDCTTICYGWVDVWVGPDGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
QY 181 EPTVTSWNSGALTSGVHTFPFAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKV 240
DB 181 EPTVTSWNSGALTSGVHTFPFAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKV 240
QY 241 DKAEPKSCDKTHTCCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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QY 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
DB 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
QY 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 476
DB 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 476

RESULT 2
US-09-948-429B-4
; Sequence 4, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
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; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-948-429B-4

Query Match      100.0%; Score 2577; DB 9; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.6e-134;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAAPRWLSQVKLQWEGGLQPSSETLSRTCVVSGSISGYIYWTWIRQT 60
DB 1 MKHLWFFLLVAAPRWLSQVKLQWEGGLQPSSETLSRTCVVSGSISGYIYWTWIRQT 60
QY 61 PGRGLEWIGHIYGNAGATTNPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVVYCARGP 120
DB 61 PGRGLEWIGHIYGNAGATTNPNLSKSRVTISKDTSKNOFFLNLSVTDADTAVVYCARGP 120
QY 121 RPDCTTICYGWVDVWVGPDGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
DB 121 RPDCTTICYGWVDVWVGPDGLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
QY 181 EPTVTSWNSGALTSGVHTFPFAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKV 240
DB 181 EPTVTSWNSGALTSGVHTFPFAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNTKV 240
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QY 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
DB 361 IEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
QY 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 476
DB 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 476

RESULT 3
US-10-124-905-12
; Sequence 12, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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GenCore version 5.1.4 p5 4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: March 29, 2003, 09:14:52 ; Search time 18.2478 Seconds  
(without alignments)  
1531.829 Million cell updates/sec

Title: US-09-758-173-4

Perfect score: 2577

Sequence: 1 MKHLWFFLLVAAPRWLSQ.....MHEALHNYTKSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA.\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	2577	100.0	476	9	US-10-124-905-4
2	2577	100.0	476	9	US-09-948-429B-4
3	2309	89.6	476	9	US-10-124-905-12
4	2309	89.6	476	9	US-09-948-429B-12
5	2103	81.6	451	9	US-09-925-179-66
6	2100	81.5	451	9	US-09-925-179-65
7	2100	81.5	451	10	US-09-920-171-14
8	2100	81.5	451	9	US-09-920-171-16
9	2099	81.5	451	9	US-09-925-179-68
10	2092	81.2	431	10	US-09-920-171-18
11	2075.5	80.5	475	10	US-09-740-002-25
12	2073	80.4	478	9	US-09-948-429B-8
13	2073	80.4	478	9	US-09-925-179-8
14	2069	80.3	453	9	US-09-925-179-8
15	2069	80.3	453	10	US-09-802-077-8
16	2069	80.3	453	10	US-09-802-096-8
17	2061.5	80.0	452	9	US-09-726-258-71
18	2047.5	79.5	475	10	US-09-740-002-27
19	2047	79.4	451	9	US-09-996-288-230

20	2045.5	79.4	450	9	US-09-996-288-216	Sequence 216, App
21	2045.5	79.4	450	9	US-09-996-288-218	Sequence 218, App
22	2045.5	79.4	450	9	US-09-996-288-250	Sequence 250, App
23	2045.5	79.4	450	10	US-09-796-848A-43	Sequence 43, Appl
24	2045.5	79.4	450	10	US-09-796-848A-49	Sequence 49, Appl
25	2044.5	79.3	450	9	US-09-996-288-220	Sequence 220, App
26	2044.5	79.3	450	9	US-09-996-288-222	Sequence 222, App
27	2044.5	79.3	450	9	US-09-996-288-224	Sequence 224, App
28	2044.5	79.3	450	10	US-09-796-848A-37	Sequence 37, Appl
29	2044.5	79.3	450	10	US-09-796-848A-39	Sequence 39, Appl
30	2044.5	79.3	450	10	US-09-796-848A-41	Sequence 41, Appl
31	2044.5	79.3	731	10	US-09-825-012-46	Sequence 46, Appl
32	2044.5	79.3	741	10	US-09-825-012-55	Sequence 55, Appl
33	2044	79.3	451	10	US-09-822-698A-26	Sequence 26, Appl
34	2042.5	79.3	450	9	US-09-996-288-232	Sequence 232, App
35	2042.5	79.3	450	9	US-09-996-288-234	Sequence 234, App
36	2042.5	79.3	450	9	US-09-996-288-236	Sequence 236, App
37	2041.5	79.2	450	9	US-09-996-288-238	Sequence 238, App
38	2041.5	79.2	450	9	US-09-996-288-242	Sequence 242, App
39	2041.5	79.2	450	9	US-09-996-288-244	Sequence 244, App
40	2041.5	79.2	450	9	US-09-996-288-246	Sequence 246, App
41	2039.5	79.1	450	9	US-09-996-288-208	Sequence 208, App
42	2039.5	79.1	729	10	US-09-825-012-52	Sequence 52, Appl
43	2039.5	79.1	739	10	US-09-825-012-61	Sequence 61, Appl
44	2038.5	79.1	450	9	US-09-996-288-210	Sequence 210, App
45	2038.5	79.1	450	9	US-09-996-288-228	Sequence 228, App

## ALIGNMENTS

## RESULT 1

US-10-124-905-4

; Sequence 4, Application US/10124905

; Patent No. US20020166136A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/124,905

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids





Db 414 LTVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSLSPGK 451

RESULT 15

US-09-296-005-16

; Sequence 16, Application US/09296005

; Patent No. 6290957

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides

; FILE REFERENCE: P1123C1r

; CURRENT APPLICATION NUMBER: US/09/296,005

; CURRENT FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 08/887,352

; EARLIER FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 26

; SEQ ID NO 16

; LENGTH: 451

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; NAME/KEY: Artificial

; LOCATION: 1-451

; OTHER INFORMATION: Heavy chain sequence derived from MAE11

US-09-296-005-16

Query Match 81.5%; Score 2100; DB 4; Length 451;

Best Local Similarity 86.5%; Pred No. 1.5e-166;

Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

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QY 80 YNPGLKSRVTISKDSKNOFFNLNSVTDADTAVYICARGPRDCTTICYGW-VDVWGP 138

Db 60 YNPVKGRTISRDDSKNTFYLQMSRAEDTAVYICARGSH-----YFGHWHFAVMGQ 113

QY 139 GDIAVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 198

Db 114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 173

QY 199 FPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNKVDKKAEPKSCDKTHTCPPC 258

Db 174 FPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHPKSNKVDKKAEPKSCDKTHTCPPC 233

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QY 379 TLPSPRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK 438

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Search completed: March 29, 2003, 09:17:41

Job time : 18.9126 secs

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QY 319 KPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVY 378  
Db 294 KPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVY 353  
QY 379 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438  
Db 354 TLPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413  
QY 439 LTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 476  
Db 414 LTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 451

RESULT 13  
US-09-109-207C-16  
; Sequence 16, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 16  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-451  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-109-207C-16

Query Match 81.5%; Score 2100; DB 4; Length 451;  
Best Local Similarity 86.5%; Pred. No. 1.5e-166;  
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

QY 20 QVKLQWEGGLQPSSETLRTCVVSGSISGYIYWTWIRQTPGRGLEWIGHIYGNATTN 79  
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNMWIRQAPGKLEWVASITVDG-STN 59  
QY 80 YNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYVCARGPRPDCTTICVGGW-VDVWGP 138  
Db 60 YNPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYVCARGSH-----YFGHWHFAVWQ 113  
QY 139 GDLVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSQVHT 198  
Db 114 GTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSQVHT 173  
QY 199 FPAVLQSSGLYLSLVVTPVSSSLGTQTYICNVNHPKNTKVDKAPKSCDKTHTCPPC 258  
Db 174 FPAVLQSSGLYLSLVVTPVSSSLGTQTYICNVNHPKNTKVDKAPKSCDKTHTCPPC 233  
QY 259 PAPELLGGPSVFLFPKPKDLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKT 318

Db 234 PAPELLGGPSVFLFPKPKDLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKT 293  
QY 319 KPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVY 378  
Db 294 KPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVY 353  
QY 379 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438  
Db 354 TLPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413  
QY 439 LTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 476  
Db 414 LTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 451

RESULT 14  
US-09-296-005-14  
; Sequence 14, Application US/09296005  
; Patent No. 6290957  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
; FILE REFERENCE: P1123C1r  
; CURRENT APPLICATION NUMBER: US/09/296,005  
; CURRENT FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 08/987,352  
; EARLIER FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 14  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-451  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-296-005-14

Query Match 81.5%; Score 2100; DB 4; Length 451;  
Best Local Similarity 86.5%; Pred. No. 1.5e-166;  
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

QY 20 QVKLQWEGGLQPSSETLRTCVVSGSISGYIYWTWIRQTPGRGLEWIGHIYGNATTN 79  
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNMWIRQAPGKLEWVASITVDG-STN 59  
QY 80 YNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYVCARGPRPDCTTICVGGW-VDVWGP 138  
Db 60 YNPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYVCARGSH-----YFGHWHFAVWQ 113  
QY 139 GDLVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSQVHT 198  
Db 114 GTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSQVHT 173  
QY 199 FPAVLQSSGLYLSLVVTPVSSSLGTQTYICNVNHPKNTKVDKAPKSCDKTHTCPPC 258  
Db 174 FPAVLQSSGLYLSLVVTPVSSSLGTQTYICNVNHPKNTKVDKAPKSCDKTHTCPPC 233  
QY 259 PAPELLGGPSVFLFPKPKDLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKT 318  
Db 234 PAPELLGGPSVFLFPKPKDLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKT 293  
QY 319 KPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVY 378  
Db 294 KPREEQYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVY 353  
QY 379 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438  
Db 354 TLPSPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 413  
QY 439 LTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 476

QY 139 GDLVTSSASTKGPSVRLPAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHT 198  
DB 114 GTLVTVSSASTKGPSVRLPAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHT 173  
QY 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVKAPKSCDKTHTCPPC 258  
DB 174 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVKAPKSCDKTHTCPPC 233  
QY 259 PAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318  
DB 234 PAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293  
QY 319 KPREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKGPREPOVY 378  
DB 294 KPREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKGPREPOVY 353  
QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSK 438  
DB 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSK 413  
QY 439 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476  
DB 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

## RESULT 11

US-08-466-151-65  
; Sequence 65, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,151  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466163  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: 08/405617  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/185899  
; FILING DATE: 26-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/879495  
; FILING DATE: 07-MAY-1992  
; PRIOR APPLICATION DATA: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-466-151-65  
Query Match 81.5%; Score 2100; DB 3; Length 451;  
Best Local Similarity 86.5%; Pred. No. 1.5e-166;  
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;  
QY 20 QVKLQOMGGELLPQSETLSRSTCVSGSGISGYVYWTIRTPGRGLEWIGHIYVNGATTN 79  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIHQAPGKLEWVASIYDVG-STN 59  
QY 80 YNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYYCARGPRPDCTTCYGGW-VDVWGP 138  
DB 60 YNPVSKGRITISRDTSKNTFYLQMNSLRRAEDTAVYYCARGSH-----YFCHWHFAVWGQ 113  
QY 139 GDLVTSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHT 198  
DB 114 GTLVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHT 173  
QY 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVKAPKSCDKTHTCPPC 258  
DB 174 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVKAPKSCDKTHTCPPC 233  
QY 259 PAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 318  
DB 234 PAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 293  
QY 319 KPREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKGPREPOVY 378  
DB 294 KPREEQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKGPREPOVY 353  
QY 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSK 438  
DB 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSK 413  
QY 439 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476  
DB 414 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451  
RESULT 12  
US-09-109-207C-14  
; Sequence 14, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 14  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-451  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-109-207C-14  
Query Match 81.5%; Score 2100; DB 4; Length 451;  
Best Local Similarity 86.5%; Pred. No. 1.5e-166;  
Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;  
QY 20 QVKLQOMGGELLPQSETLSRSTCVSGSGISGYVYWTIRTPGRGLEWIGHIYVNGATTN 79  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIHQAPGKLEWVASIYDVG-STN 59

Db 175 EPTVSMNSGALTSVHTPVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKV 234

Qy 241 DKAEPKSCDKTHTCPAPPELLGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDP 300

Db 235 DKVESK--YGPCCSCAPFEGGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDP 291

Qy 301 EVKFNMYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAP 360

Db 292 EVQFNMYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAP 351

Qy 361 IEXTISKAGOPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420

Db 352 IEXTISKAGOPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 411

Qy 421 KTTTPVLDSDGSPFLYSLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 476

Db 412 KTTTPVLDSDGSPFLYSLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 467

RESULT 9

US-08-887-352B-14

; Sequence 14, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-887-352B-14

Query Match 81.5%; Score 2100; DB 2; Length 451;

Best Local Similarity 86.5%; Pred. No. 1.5e-166;

Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

Qy 20 QVKLQWGGELQLQPSSTLSRTCVSGSGISGYVYWTWIRQTPGRLGLEWIGHYNGATTN 79

Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASIYDG-STN 59

Qy 80 YNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYVCARGPRPDCTTCYCGWM-VDVWGP 138

Db 60 YNPVSVKGRITISRDDSKNTFYQLQMSLRAEDTAVYVCARGSH-----YFGWHFAVWGQ 113

Qy 139 GDLVTVSSASTKGPSVFFLAPSSKSTSGTAAALGCLVKDYPPEPVTVSMNSGALTSVHT 198

Db 114 GLTVTVSSASTKGPSVFFLAPSSKSTSGTAAALGCLVKDYPPEPVTVSMNSGALTSVHT 173

Qy 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVKKABPKSCDKTHTCPCC 258

Db 174 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVKKABPKSCDKTHTCPCC 233

Qy 259 PABELLGGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318

Db 234 PABELLGGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293

Qy 319 KPREEQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 378

Db 294 KPREEQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 353

Qy 379 TLPSPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSLK 438

Db 354 TLPSPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSLK 413

Qy 439 LTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 476

Db 414 LTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 451

RESULT 10

US-08-887-352B-16

; Sequence 16, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-887-352B-16

Query Match 81.5%; Score 2100; DB 2; Length 451;

Best Local Similarity 86.5%; Pred. No. 1.5e-166;

Matches 396; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

Qy 20 QVKLQWGGELQLQPSSTLSRTCVSGSGISGYVYWTWIRQTPGRLGLEWIGHYNGATTN 79

Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASIYDG-STN 59

Qy 80 YNPSLKSRVTISKDTSKNQFFLNLSVTDADTAVYVCARGPRPDCTTCYCGWM-VDVWGP 138

Db 60 YNPVSVKGRITISRDDSKNTFYQLQMSLRAEDTAVYVCARGSH-----YFGWHFAVWGQ 113

## RESULT 7

US-08-397-411-7  
; Sequence 7, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/397,411  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/859,583  
; FILING DATE: 27-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 011823-004901  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 446 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-397-411-7

Query Match 81.7%; Score 2106.5; DB 3; Length 446;  
Best Local Similarity 88.2%; Pred. No. 4.1e-167;  
Matches 403; Conservative 16; Mismatches 27; Indels 11; Gaps 4;  
QY 20 QVQLQWGGELGQSPETLSRSCVSGSGTSISGVYVYVWIRQTPGRGLEWIGHYNGATTN 79  
DB 1 QVQLQESGPGGLVAPSETLSLTCTVSGFSLTNGV-HWVRQSPGKLEWIG-VKWSGGSTE 58  
QY 80 YNPSLKRVTISKDTSKNQPFNLNSVTDADTAVYYCARGPRPDCTTICYGWVDVWVG 139  
DB 59 YNAAFISRLTISKDTSKNQVSLKSLNLTADTAVYYCARNDR-----YA--MDYWGQ 109  
QY 140 DLTVVSSATKGPSVPLAPSSKSTSGGTAALGCLVKDYFPPVPTVSNVNSGALTSGVHTF 199  
DB 110 TLTVVSSATKGPSVPLAPSSKSTSGGTAALGCLVKDYFPPVPTVSNVNSGALTSGVHTF 169  
QY 200 PAVLQSGGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKAEPKSCDKTHTCCPCP 259  
DB 170 PAVLQSGGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKAEPKSCDKTHTCCPCP 229  
QY 260 APELLGGPSVFLPDKPKOTLMTSRTPETVTCVVDVSHEDDPEVKFNWYVDGVVHNNAKTK 319  
DB 230 APELLGGPSVFLPDKPKOTLMTSRTPETVTCVVDVSHEDDPEVKFNWYVDGVVHNNAKTK 289

QY 320 PREQVNSTYRVSVLTIVLHQDLNGLKEYCKVSNKALPAPIEKTISKAKGQPREPQVYT 379  
DB 290 PREQVNSTYRVSVLTIVLHQDLNGLKEYCKVSNKALPAPIEKTISKAKGQPREPQVYT 349  
QY 380 LPPSRDELTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKL 439  
DB 350 LPPSRDELTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKL 409  
QY 440 TVDKSRWQOGNVFSCVMHEALHNHYTOKSLSPGK 476  
DB 410 TVDKSRWQOGNVFSCVMHEALHNHYTOKSLSPGK 446

## RESULT 8

US-08-523-894-10  
; Sequence 10, Application US/08523894  
; Patent No. 6136310  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; TITLE OF INVENTION: Therapy  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314-3187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/523,894  
; FILING DATE: 06-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 467 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-523-894-10

Query Match 81.7%; Score 2104.5; DB 4; Length 467;  
Best Local Similarity 84.2%; Pred. No. 6.5e-167;  
Matches 401; Conservative 24; Mismatches 42; Indels 9; Gaps 2;  
QY 1 MKHLWFFLLVAAPRWLSOVKLOQWGGELGQSPETLSRSCVSGSGTSISGVYVYVWIRQ 60  
DB 1 MKHLWFFLLVAAPRWLSOVKLOQWGGELGQSPETLSRSCVSGSGTSISGVYVYVWIRQ 60  
QY 61 PGRGLEWIGHYNGATTNYPNPSLKRVTISKDTSKNQPFNLNSVTDADTAVYYCARGP 120  
DB 61 PGRGLEWIGHYNGATTNYPNPSLKRVTISKDTSKNQPFNLNSVTDADTAVYYCARGP 117  
QY 121 RDCCTTCYCGWVDVWVGDLVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYF 180  
DB 121 RDCCTTCYCGWVDVWVGDLVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYF 174  
QY 181 EPVTVSNVNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTK 240  
DB 181 EPVTVSNVNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTK 240

NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/523,894  
FILING DATE: 06-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-6620  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-523-894-12

Query Match 82.0%; Score 2112.5; DB 4; Length 467;  
Best Local Similarity 84.5%; Pred. No. 1.4e-167;  
Matches 402; Conservative 24; Mismatches 41; Indels 9; Gaps 2;

QY 1 MKHLWFFLLVAAPRWLSQVKLQWQEGGLQPSVTLRTCTCVVSGGSGYGYWTWIROT 60  
DB 1 MKHLWFFLLVAAPRWLSQVKLQWQEGGLQPSVTLRTCTCVVSGGSGYGYWTWIROT 60  
QY 61 PGRGLEWIGHIYNGGATTNNPSLKRVTISKDTSKNQFFLNLSVTDADTAVYYCARGP 120  
DB 61 PGRGLEWIGHIYNGGATTNNPSLKRVTISKDTSKNQFFLNLSVTDADTAVYYCA--- 117  
QY 121 RPDCTTICYGWVDVWPGDLVTVSSASTKGPSPVPLAPSSKSTSGTAAALGCLVKDYFP 180  
DB 118 ---SNILKYLHLLYMGQGVLTVSSASTKGPSPVPLAPSSKSTSGTAAALGCLVKDYFP 174  
QY 181 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKV 240  
DB 175 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKV 234  
QY 241 DKAEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300  
DB 235 DKRVESK---YGPCCPCPAPEFEGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 291  
QY 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAP 360  
DB 292 EVQFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAP 351  
QY 361 IEKTIKAKQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420  
DB 352 IEKTIKAKQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 411  
QY 421 KTTTPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 476  
DB 412 KTTTPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSLGK 467

RESULT 6

US-08-523-894-8  
; Sequence 8, Application US/08523894  
; Patent No. 6136310

GENERAL INFORMATION:  
APPLICANT: Hanna, Nabil  
APPLICANT: Newman, Roland A.  
APPLICANT: Reff, Mitchell E.  
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
TITLE OF INVENTION: Therapy  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/523,894  
FILING DATE: 06-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-6620  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-523-894-8

Query Match 81.9%; Score 2111.5; DB 4; Length 467;  
Best Local Similarity 84.5%; Pred. No. 1.7e-167;  
Matches 402; Conservative 24; Mismatches 41; Indels 9; Gaps 2;

QY 1 MKHLWFFLLVAAPRWLSQVKLQWQEGGLQPSVTLRTCTCVVSGGSGYGYWTWIROT 60  
DB 1 MKHLWFFLLVAAPRWLSQVKLQWQEGGLQPSVTLRTCTCVVSGGSGYGYWTWIROT 60  
QY 61 PGRGLEWIGHIYNGGATTNNPSLKRVTISKDTSKNQFFLNLSVTDADTAVYYCARGP 120  
DB 61 PGRGLEWIGHIYNGGATTNNPSLKRVTISKDTSKNQFFLNLSVTDADTAVYYCA--- 117  
QY 121 RPDCTTICYGWVDVWPGDLVTVSSASTKGPSPVPLAPSSKSTSGTAAALGCLVKDYFP 180  
DB 118 ---SNILKYLHLLYMGQGVLTVSSASTKGPSPVPLAPSSKSTSGTAAALGCLVKDYFP 174  
QY 181 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKV 240  
DB 175 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKV 234  
QY 241 DKAEPKSCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 300  
DB 235 DKRVESK---YGPCCPCPAPEFEGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDP 291  
QY 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAP 360  
DB 292 EVQFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAP 351  
QY 361 IEKTIKAKQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420  
DB 352 IEKTIKAKQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 411  
QY 421 KTTTPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 476  
DB 412 KTTTPVLDSDGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSLGK 467

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANTCUT01  
CLONE: 1513264  
US-09-049-672A-4

Query Match 88.4%; Score 2277.5; DB 4; Length 473;  
Best Local Similarity 90.8%; Pred. No. 2.7e-181;  
Matches 434; Conservative 16; Mismatches 21; Indels 7; Gaps 4;  
QY 1 MKHLWFFLLVAAPRWLVLSQVQLQWGEGLQPSLRTCTCVVSGSI-SGYYYWTWIRQ 59  
DB 1 MKHLWFFLLVAAPRWLVLSQVQLQWGEGLQPSLRTCTCAVSGSITSGGYWWSWIRQ 60  
QY 60 TPGRLGIEWHGYGNATTNYPNLSKRVTSKDTSKNQFFLNLSVTDADTAVYYCAR 119  
DB 61 PPGKLGIEWHGYGNATTNYPNLSKRVTSKDTSKNQFFLNLSVTDADTAVYYCAR 118  
QY 120 PRDCTTCYGVG-VDMWPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 178  
DB 119 ---DVLGRGGNMDVWGQGLTTLVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 175  
QY 179 FPEPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNT 238  
DB 176 FPEPVTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNT 235  
QY 239 KVDKKAEPKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE 298  
DB 236 KVDKRVPEKSCDKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE 295  
QY 299 DPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALP 358  
DB 296 DPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALP 355  
QY 359 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 418  
DB 356 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 415  
QY 419 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQOGNVPFSCVMHEALHNHYTQKSLSLSPGK 476  
DB 416 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQOGNVPFSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 4  
US-08-793-450-8  
Sequence 8, Application US/08793450  
Patent No. 6312690  
GENERAL INFORMATION:  
APPLICANT: EDELMAN, LENA  
APPLICANT: MARGARITTE, CHRISTEL  
APPLICANT: KACZOREK, MICHEL  
APPLICANT: CHAABTHI, HASSAN  
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,450  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
FILING DATE: 02-SEP-1994  
APPLICATION NUMBER: FR 94/10566  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 472 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-450-8  
Query Match 85.6%; Score 2206; DB 4; Length 472;  
Best Local Similarity 90.0%; Pred. No. 2.4e-175;  
Matches 422; Conservative 9; Mismatches 34; Indels 4; Gaps 3;  
QY 8 LLLVAAPRWLVLSQVQLQWGEGLQPSLRTCTCVVSGSISGYYYWTWIRQTPGRGLEW 67  
DB 8 LFLVATATGTVHSGVQLQWGEGLQPSLRTCTCVVSGFSG-YWMSWIRQPPGKLEW 66  
QY 68 IGHLYGNGATTNYPNLSKRVTSKDTSKNQFFLNLSVTDADTAVYYCARGRPDCDTTI 127  
DB 67 IGEINHSQ-STNYPNLSKRVTSKDTSKNQFFLNLSVTDADTAVYYCARA--PEYKWK 123  
QY 128 CYGQWVDWPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 187  
DB 124 YHGDMFDPWGGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 183  
QY 188 NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKAEPK 247  
DB 184 NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKAEPK 243  
QY 248 SCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY 307  
DB 244 SCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY 303  
QY 308 VDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKTISK 367  
DB 304 VDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKTISK 363  
QY 368 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL 427  
DB 364 AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL 423  
QY 428 DSDGSFFLYSKLTVDKSRWQOGNVPFSCVMHEALHNHYTQKSLSLSPGK 476  
DB 424 DSDGSFFLYSKLTVDKSRWQOGNVPFSCVMHEALHNHYTQKSLSLSPGK 472  
RESULT 5  
US-08-523-894-12  
Sequence 12, Application US/08523894  
Patent No. 6136310  
GENERAL INFORMATION:  
APPLICANT: Hanna, Nabil  
APPLICANT: Newman, Roland A.  
APPLICANT: Reff, Mitchell E.  
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
COMPUTER READABLE FORM:



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QY 61 PGRGLEWIGHIYNGGATTNNPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYICARGP 120
DB 61 PGRGLEWIGHIYNGGATTNNPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYICARGP 120
QY 121 RPDCTTICYGWVDVNGPDLVTVSSASTKGPVFPFLAPSSKSTSGTAAALGCLVKDYFP 180
DB 121 RPDCTTICYGWVDVNGPDLVTVSSASTKGPVFPFLAPSSKSTSGTAAALGCLVKDYFP 180
QY 181 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKV 240
DB 181 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKV 240
QY 241 DKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 301 EVKFNWYVDGVEVHNAKTKPRBEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNAKTKPRBEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
QY 361 IEKTSKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTSKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
QY 421 KTTPPVLDSDGSGFFLYSKLTVDKSRWQOQGVFSCSVNHEALHNHYTKLSLSLSPGK 476
DB 421 KTTPPVLDSDGSGFFLYSKLTVDKSRWQOQGVFSCSVNHEALHNHYTKLSLSLSPGK 476

RESULT 2
US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-12

Query Match 89.6%; Score 2309; DB 3; Length 476;
Best Local Similarity 91.2%; Pred. No. 6.6e-184;
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Matches 434; Conservative 9; Mismatches 33; Indels 0; Gaps 0;
QY 1 MKHLWFFLLVAAPRWYLSQVKLQOMGEGLLQFSETLSRTCVVSGGSGISGYIYTWIRQT 60
DB 1 MKHLWFFLLVAAPRWYLSQVKLQOMGEGLLQFSETLSRTCVVSGGSGISGYIYTWIRQT 60
QY 61 PGRGLEWIGHIYNGGATTNNPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYICARGP 120
DB 61 PGRGLEWIGHIYNGGATTNNPSLKSRTVTSKDTSKNQFFLNLSVTDADTAVYICARGP 120
QY 121 RPDCTTICYGWVDVNGPDLVTVSSASTKGPVFPFLAPSSKSTSGTAAALGCLVKDYFP 180
DB 121 RPDCTTICYGWVDVNGPDLVTVSSASTKGPVFPFLAPSSKSTSGTAAALGCLVKDYFP 180
QY 181 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKV 240
DB 181 EPTVTSWNSGALTSVGHVTPPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKV 240
QY 241 DKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
DB 241 DKAEPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 301 EVKFNWYVDGVEVHNAKTKPRBEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
DB 301 EVKFNWYVDGVEVHNAKTKPRBEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
QY 361 IEKTSKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
DB 361 IEKTSKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
QY 421 KTTPPVLDSDGSGFFLYSKLTVDKSRWQOQGVFSCSVNHEALHNHYTKLSLSLSPGK 476
DB 421 KTTPPVLDSDGSGFFLYSKLTVDKSRWQOQGVFSCSVNHEALHNHYTKLSLSLSPGK 476

RESULT 3
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
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GenCore version 5.1.4.p5 4578  
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 16.9126 Seconds  
(without alignments)  
828.100 Million cell updates/sec

Title: US-09-758-173-4

Perfect score: 2577

Sequence: 1 MKHLWFFLLVAAPRWLSQ.....MHEALHNYTKSLSPGK 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2.6/prodata/1/1aa/5B-COMB.pep:\*

3: /cgn2.6/prodata/1/1aa/6A-COMB.pep:\*

4: /cgn2.6/prodata/1/1aa/6B-COMB.pep:\*

5: /cgn2.6/prodata/1/1aa/PCTUS-COMB.pep:\*

6: /cgn2.6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2577	100.0	476	3	US-08-487-550-4
2	2309	89.6	476	3	US-08-487-550-12
3	2277.5	88.4	473	4	US-09-049-672A-4
4	2206	85.6	472	4	US-08-793-450-8
5	2112.5	82.0	467	4	US-08-523-894-12
6	2111.5	81.9	467	4	US-08-523-894-8
7	2106.5	81.7	446	3	US-08-397-411-7
8	2104.5	81.7	467	4	US-08-523-894-10
9	2100	81.5	451	2	US-08-887-352B-14
10	2100	81.5	451	2	US-08-887-352B-16
11	2100	81.5	451	3	US-08-466-151-65
12	2100	81.5	451	4	US-09-109-207C-14
13	2100	81.5	451	4	US-09-109-207C-16
14	2100	81.5	451	4	US-09-296-005-14
15	2100	81.5	451	4	US-09-296-005-16
16	2092	81.2	451	2	US-08-887-352B-18
17	2092	81.2	451	4	US-09-109-207C-18
18	2092	81.2	451	4	US-09-282-505-2
19	2092	81.2	451	4	US-09-054-255-2
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21	2073	80.4	478	3	US-08-487-550-8
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29	2032.5	78.9	449	4	US-09-679-397-2	Sequence 2, Appl
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34	1997.5	77.5	467	4	US-09-049-672A-8	Sequence 8, Appl
35	1978	76.8	472	4	US-09-301-593-43	Sequence 43, Appl
36	1976.5	76.7	453	4	US-09-301-593-18	Sequence 18, Appl
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38	1961	76.1	711	4	US-09-485-737B-90	Sequence 90, Appl
39	1960.5	76.1	454	2	US-07-934-373C-22	Sequence 22, Appl
40	1960.5	76.1	454	3	US-08-437-642B-22	Sequence 22, Appl
41	1960.5	76.1	454	4	US-08-146-206C-22	Sequence 22, Appl
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44	1949	75.6	451	4	US-09-466-635-3	Sequence 3, Appl
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ALIGNMENTS

RESULT 1

US-08-487-550-4

; Sequence 4, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; NUMBER OF INVENTIONS: IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-487-550-4

Query Match 100.0%; Score 2577; DB 3; Length 476;

Best Local Similarity 100.0%; Pred. No. 3.5e-206;

Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
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LOCUS
DEFINITION
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720 bp DNA linear PAT 31-JAN-2002
Human monoclonal antibody against parathyroid hormone-related
protein Human monoclonal antibody against parathyroid
hormone-related protein Human monoclonal antibody against
parathyroid hormone-related protein Human monoclonal antibody
against parathyroid hormone-related protein Human monoclonal
antibody against parathyroid hormone-related protein Human
monoclonal antibody against parathyroid hormone-related protein.
ACCESSION
E35204
VERSION
E35204.1 GI:18624432
KEYWORDS
JP 2000080100-A/4.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 720)
AUTHORS
Hori,N., Kusunoki,C. and Kamata,M.
TITLE
Human monoclonal antibody against parathyroid hormone-related
JOURNAL
Patent: JP 2000080100-A 4 21-MAR-2000;
JAPAN TOBACCO INC
COMMENT
OS Homo sapiens (human)
.PN JP 2000080100-A/4
.FD 21-MAR-2000
.PF , 12-OCT-1998 JP 1998304793
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PI NOBUAKI HORI, CHIRO KUSUNOKI, MASASHI KAWATA
PC C07K16/26, A61K31/00, A61K31/00, A61K31/00, A61K31/00,
PC A61K31/00,
PC A61K39/395, A61K39/395, C12N5/10, C12N15/02, C12P21/08, // C12N5/10,
PC C12R1:91,
PC C12N15/02, C12R1:91, (C12P21/08, C12R1:91), C12N5/00, C12N15/00,
PC (C12N5/00, C12R1:91), (C12N15/00, C12R1:91)
CC
FH
FT CDS Location/Qualifiers
FT sig_peptide (1)..(720)
FT V_region (61)..(397)
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/db_xref="taxon:9606"
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AUTHORS	1 (bases 1 to 720)	
TITLE	Hori,N., Kusunoki,C. and Kamata,M.	
JOURNAL	Human monoclonal antibody against parathyroid hormone-related Patent: JP 200080100-A 7 21-MAR-2000;	
COMMENT	JAPAN TOBACCO INC	
	OS Homo sapiens (human)	
	PN JP 200080100-A/7	
	PD 21-MAR-2000	
	PF 12-OCT-1998 JP 1998304793	
	PR	
	PI NOBUAKI HORI, CHIHIRO KUSUNOKI MASASHI KAMATA	
	PC C07K16/26,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,	
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	PC A61K39/395,A61K39/395,C12N5/10,C12N15/02,C12P21/08/((C12N5/10,	
	PC C12R1:91),	
	PC (C12N15/02,C12R1:91),(C12P21/08,C12R1:91),C12N5/00,C12N15/00,	
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	Matches 642; Conservative 0; Mismatches 76; Indels 0; Gaps 0;	
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RESULT 11
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LOCUS Human monoclonal antibody against parathyroid hormone-related protein.
DEFINITION E35205 Human monoclonal antibody against parathyroid hormone-related protein.
ACCESSION E35205
VERSION E35205.1 Gi:18624433
KEYWORDS JP 2000080100-A/5.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 720)
Hori,N., Kusunoki,C. and Kamata,M.
TITLE Human monoclonal antibody against parathyroid hormone-related
JOURNAL Patent: JP 2000080100-A 5 21-MAR-2000;
JAPAN TOBACCO INC
COMMENT OS Homo sapiens (human)
PN JP 2000080100-A/5
PD 21-MAR-2000
PF 12-OCT-1998 JP 1998304793
PR
PI NORUAKI HORI, CHIHIRO KUSUNOKI, MASASHI KAMATA
PC C07K16/26,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,
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BASE COUNT 174 a 190 c 188 g 163 t 5 others
ORIGIN
Query Match 83.2%; Score 599.4; DB 6; Length 720;
Best Local Similarity 89.4%; Pred.No.5e-163; Indels 0; Gaps 0;
Matches 642; Conservative 0; Mismatches 76;
Qy 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60
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RESULT 12
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LOCUS Human monoclonal antibody against parathyroid hormone-related protein.
DEFINITION E35207 Human monoclonal antibody against parathyroid hormone-related protein.
ACCESSION E35207
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DEFINITION AX067347  
ACCESSION AX067347.1 GI:12544971  
VERSION  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Yuqiu, J. and Mitcham, J.L.  
JOURNAL Compositions and methods for the therapy and diagnosis of breast  
PATENT: WO 0078960-A 51 28-DEC-2000;  
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DEFINITION AB064106  
ACCESSION AB064106  
VERSION AB064106.1 GI:21669418  
KEYWORDS  
SOURCE Homo sapiens cDNA to mRNA, clone\_lib:AIMS4 clone:K65.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,  
Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,  
Miura, K. and Kurosawa, Y.  
JOURNAL Construction and characterization of antibody libraries: isolation  
of therapeutic human antibodies and application to functional  
genomics  
Unpublished  
REFERENCE 2 (bases 1 to 830)  
AUTHORS Kurosawa, Y.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for  
Comprehensive Medical Science, Fujita Health University;  
Kutsukake-cho, Toyoake 470-1192, Japan  
(E-mail: kurosawa@fujita-hu.ac.jp, tel:81-562-93-9387)  
COMMENT Please visit our web site  
URL: http://www.fujita-hu.ac.jp/immunity/.  
FEATURES  
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/notes="peB signal peptide"  
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Best Local Similarity 91.5%; Pred. No. 4.4e-163;  
Matches 635; Conservative 0; Mismatches 59; Indels 0; Gaps 0;  
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QY 85 CTGTCCCTTCCCATCACACTGGAGAGCGCGCTCCATCTCTCTGTTAGTCTAGTCAAAGC 144  
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DEFINITION Homo sapiens, clone MGC:22745 IMAGE:4251290, mRNA, complete cds.
ACCESSION BC030814
VERSION BC030814.1 GI:21410816
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 972)
Strausberg, R.
Direct Submission
Submitted (03-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov
Series: IRAL Plate: 35 Row: e Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomeScan gene prediction, Similarity but not identity
to protein.
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Query Match 84.4%; Score 607.6; DB 9; Length 972;
Best Local Similarity 90.4%; Pred. No. 2.1e-165;
Matches 649; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
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 DEFINITION Antihuman Fas humanized antibody-containing antirheumatic.  
 ACCESSION E40697  
 VERSION E40697.1 GI:18627286  
 KEYWORDS JP 2000154149-A/68.  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 720)  
 AUTHORS Srizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.  
 TITLE Antihuman Fas humanized antibody-containing antirheumatic  
 JOURNAL Patent: JP 2000154149-A 68 06-JUN-2000;  
 SANKYO CO LTD  
 COMMENT OS Artificial Sequence  
 PN JP 2000154149-A/68  
 PD 06-JUN-2000  
 PF 17-SEP-1999 JP 1999263984  
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 PI NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI KAORI NAKAHARA,  
 PI SHIN YONEHARA  
 PC A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00  
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 Best Local Similarity 91.4%; Pred. No. 1.2e-168;  
 Matches 656; Conservative 0; Mismatches 62; Indels 0; Gaps 0;  
 QY 1 ATGAGCTCCCTGCTCAGCTCCCTGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60  
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Qy	661	GTACCCATCAGGGCCTGAGCTCGGCCCTCAAAAGAGCTTCAACAGGGGAGAGTGTT	718
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LOCUS	E40695	Antihuman Fas humanized antibody-containing antirheumatic.	
DEFINITION	E40695		
ACCESSION	E40695	1 GI:19627284	
VERSION	JP 2000154149-A/66.	synthetic construct.	
KEYWORDS		synthetic construct	
SOURCE		artificial sequences.	
ORGANISM		1 (bases 1 to 720)	
REFERENCE		Srizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.	
AUTHORS		Antihuman Fas humanized antibody-containing antirheumatic	
TITLE		Patent: JP 2000154149-A 66 06-JUN-2000;	
JOURNAL		SANKYO CO LTD	
COMMENT		OS Artificial Sequence	
		PN JP 2000154149-A/66	
		PD 06-JUN-2000	
		PF 17-SEP-1999 JP 1999263984	
		PI NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI KAORI NAKAHARA,	
		PI SHIN YONEHARA	
		PC A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00	
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461	CUAAATACATCTTATCCAGAGAGGCGAAAGTACAGTGGAAAGTGGATAACGCCCTCCAA	540
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501	TCGGGTAACTCTCCAGGAGAGTGTCTACAGAGCAGGACAGCAAGGACAGCACCTTACAGCCTC	580
521	TCGGGTAACTCTCCAGGAGAGTGTCTACAGAGCAGGACAGCAAGGACAGCACCTTACAGCCTC	600
541	AGCAGACCTCTGACGCTTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCCGAA	620
561	AGCAGACCTCTGACGCTTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCCGAA	640
581	GTCAACCATCAGGGCCTTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT	660
601	GTCAACCATCAGGGCCTTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT	680

RESULT	4
ELOCUS	E40748
DEFINITION	891 bp DNA linear PAT 31-JAN- Antihuman Fas humanized antibody-containing antirheumatic.
ACCESSION	E40748
VERSION	E40748.1 GI:18627337
KEYWORDS	JP 2000154149-A/119.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 891)
AUTHORS	Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yoneha-
TITLE	Antihuman Fas humanized antibody-containing antirheumatic
JOURNAL	Patent: JP 2000154149-A 119 06-JUN-2000; SANKYO CO LTD
COMMENT	OS Homo sapiens (human) PN JP 2000154149-A/119 ED 06-JUN-2000

PF	17-SEP-1999	JP	1999263984	
PR				
PI	NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, WATARU TAKAHASHI, PI			
	NAKAHARA,			
PI	SHIN YONSHARA			
PC	A61K39/395, A61P29/00, C12N15/09, C07K16/28, C12P21/02, C12N1			
CC				
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	source			

source  
1. '891

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Best Local Similarity 100.0%; Pred. No. 4.5e-198;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 661 GTCACCCATCAGGCGCTCAGCTCGCGCTCAAGAGCTTCAACAGGGAGAGTGTGA 720

RESULT 2
BC022362          973 bp   mRNA   linear   PRI 04-FEB-2002
LOCUS             Homo sapiens, clone MGC:23888 IMAGE:4704496, mRNA, complete cds.
DEFINITION        BC022362
ACCESSION         BC022362
VERSION           BC022362.1 GI:18490210
KEYWORDS          MGC.
SOURCE            Homo sapiens.
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1 (bases 1 to 973)
AUTHORS           Strausberg, R.
TITLE             Direct Submission
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JOURNAL
REMARK
COMMENT
Submitted (01-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 37 Row: b Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
FEATURES             Location/Qualifiers
  source              1..973
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                        /db_xref="taxon:9606"
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                        /clone_lib="NIH_MGC_77"
                        /lab_host="DH10B"
                        /note="Vector: pDNR-LIB"
                        31..750
                        /codon_start=1
                        /product="Unknown (protein for MGC:23888)"
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                        /db_xref="GI:18490211"
                        /translation="MRLPAQLLLMLWPGSSGDVMTQSPSLPVLTPGPAISICR
                        STQSLVSDGNTYLNWFGREGSPRRLLIYKVNDRSDVDPDRFSGSGGDTFLTKITR
                        VEADVGVIYFCMQGTHWSPSTFGQGLKEIKETVAAPSFIIPPSDEQLKSTASVCL
                        LNNFYPRKAVQWKVDNALQSNQESVTEQDSKDSYLSLTLSKADYKHKVYA
                        CEVTHQGLSSPVTYSFNRGEC"
BASE COUNT          249 a   279 c   229 g   216 t
ORIGIN
Query Match          87.3%; Score 628.4; DB 9; Length 973;
Best Local Similarity 92.2%; Pred. No. 1.9e-171;
Matches 662; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 1 ATGAGCTCTCTCTCAGCTCTCTGCGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60
Db 31 ATGAGCTCTCTCTCAGCTCTCTGCGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 90
QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACCTTGGAGAGCGGCGCTCC 120
Db 91 GATGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACCTTGGAGAGCGGCGCTCC 150
QY 121 ATCTCTGTAGTCTAGTCAAAAGCCTTAAACACAGTAATGGAGACACCTTCTGTAGTTGG 180
Db 151 ATCTCTGTAGTCTAGTCAAAAGCCTTAAACACAGTAATGGAGACACCTTCTGTAGTTGG 210
QY 181 TATCAGCAGAACCCAGGCGCAACTCCCAAGGCTCTCTGATTATTAAGGTTTCTTAACCGGAC 240
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Db 271 TCTGGGCTCCACAGACAGATTACGCGGCGAGTGGGCGAGGACAGATTTTCACACTGAAATC 330
QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGTTTATTTCTCGGGCGAGGTACAAGGACTCCT 360
Db 331 ACCAGGGTGGAGGCTGAGGATGTTGGGTTTATTTCTCATGTCAGGGGTACACACTGGCGC 390
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:05 ; Search time 2259.24 Seconds  
(without alignments)  
9274.790 Million cell updates/sec

Title: US-09-758-173-5  
Perfect score: 720  
Sequence: 1 ATGAGCCCTCCCTGCTCAGCT.....TCAACAGGGAGAGGTTTGA 720

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

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16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

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20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

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39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	720	100.0	720	6	AR108864	AR108864 Sequence
2	628.4	87.3	973	9	BC022362	BC022362 Homo sapi
3	622	86.4	720	6	E40698	E40698 Antihuman F
4	620.4	86.2	891	6	E40748	E40748 Antihuman F
5	618.8	85.9	720	6	E40696	E40696 Antihuman F
6	618.8	85.9	720	6	E40697	E40697 Antihuman F
7	617.2	85.7	720	6	E40695	E40695 Antihuman F
8	607.6	84.4	972	9	BC030814	BC030814 Homo sapi
9	601.2	83.5	963	6	AX067347	AX067347 Sequence
10	599.6	83.3	830	9	AB064106	AB064106 Homo sapi
11	599.4	83.2	720	6	E35205	E35205 Human monoc
12	599.4	83.2	720	6	E35208	E35208 Human monoc
13	598.8	83.2	720	6	E35204	E35204 Human monoc
14	598.2	83.1	720	6	E35201	E35201 Homo sapi
15	598	83.1	830	9	AB064102	AB064102 Homo sapi
16	596.6	82.9	720	6	E35206	E35206 Human monoc
17	595.4	82.7	720	6	E35203	E35203 Human monoc
18	593.4	82.4	720	6	E35202	E35202 Human monoc
19	591.6	82.2	720	6	E35202	E35202 Human monoc
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23	587.8	81.6	720	6	E35210	E35210 Human monoc
24	583.4	81.0	786	9	AB064059	AB064059 Homo sapi
25	580.4	80.6	794	9	AB064137	AB064137 Homo sapi
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33	566	78.6	828	9	AB064104	AB064104 Homo sapi
34	564.4	78.4	785	9	AB064054	AB064054 Homo sapi
35	561.2	77.9	726	6	E10698	E10698 cDNA encodi
36	561.2	77.9	785	9	AB064055	AB064055 Homo sapi
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45	532	73.9	660	6	AX277240	AX277240 Sequence

ALIGNMENTS

RESULT 1  
AR108864 LOCUS AR108864 720 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 5 from patent US 6113898.  
ACCESSION AR108864  
VERSION AR108864.1 GI:12825140  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 720)  
AUTHORS Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.  
TITLE Human B7.1-specific primatized antibodies and transfectomas  
expressing said antibodies  
JOURNAL Patent: US 6113898-A 5 05-SEP-2000;



Db 241 TCCGGGGTCCCTGACAGGTTCACTGTCAGTGGATCAGGCACAGATTTTACACTGAAAATC 300  
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Db 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTTCTGCGGCAAGGTACAAAGGACTCCT 360  
Qy 361 CCCACTTTCGGGGGAGGAGCCAAAGGTGGAAATCAACGTAAGTGGCTGGCAACCATCTGTC 420  
Db 361 TTCACCTTTCGGGGGCTGGGAGCCAAAGTGGATATCAACGTAAGTGGCTGGCAACCATCTGTC 420  
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Db 421 TTCATCTTCCCGCCATNTGATGAGCAGTTGAAATCTGGAACTGCGCTCTGTTGTGTCCTG 480  
Qy 481 CTGAATAACTTCTATCCCGAGAGGCAAGGTACAGTGGAGGTGGATTAACGCCCTCCAA 540  
Db 481 CTGAATAACTTCTATCCCGAGAGGCAAGGTACAGTGGAGGTGGATTAACGCCCTCCAA 540  
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Db 601 AGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGGGAA 660  
Qy 661 GTCACCCATCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718  
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Search completed: April 5, 2003, 20:19:19  
Job time : 198.594 secs



XX Yuiqu J, Mitcham JL;  
 XX WPI; 2001-041426/05.  
 XX New polynucleotides encoding breast tumor specific proteins, useful for  
 XX prevention, treatment and diagnosis of breast cancer -  
 XX Claim 25; Page 135-136; 165pp; English.  
 XX The present invention provides the coding sequences for a number of  
 XX breast cancer related proteins. These can be used in vaccinations  
 XX against, diagnosis of and treatment of cancer, particularly breast  
 XX cancer.  
 XX Sequence 963 BP; 253 A; 264 C; 224 G; 213 T; 9 other;  
 SQ  
 Query Match 83.5%; Score 601.2; DB 22; Length 963;  
 Best Local Similarity 89.8%; Pred. No. 1.5e-150;  
 Matches 645; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
 QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTCGCTCGGTCCTCGGGTCCAGTGGG 60  
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 DB 123 ATCTCTGTAGTGTAGTCAAGCCTTAAACACAGTAAATGGAGATACAGTATTGGATTGG 182  
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 DB 183 TACCTGCAGAGCCAGGACAGTCTCCACAGCTCCTGATCTATTGGCTTCTAAGCGGGCC 242  
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 DB 243 TCGGGGTTCCAGACAGATTTCAGGCGAGTGGGGAGGAGGACAGATTTCACACTGAAATTC 302  
 QY 301 AGCGAGTGGAGGCTGAAGATGTGTGGGGTTTATTTCTCGGGGCAAGGTACAAGGACTCTCT 360  
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 QY 361 CCACATTTTCGGCGGAGGAGCAAGAGTGGAAATCAAAACGTACGGTGGCTGCACCATCTGTC 420  
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 DB 663 GTACCCATCAGGCGCTGAGCTGCCCGTCAACAAAGCTTCAACAGGGGAGTGT 720

RESULT 15

AAAL3924

ID AAAL3924 standard; DNA; 720 BP.

XX AAAL3924;  
 AC 02-AUG-2000 (first entry)  
 DT Human PTHrP monoclonal antibody clone 2F8-10-3 DNA SEQ ID NO:11.  
 DE Human PTHrP monoclonal antibody clone 2F8-10-3 DNA SEQ ID NO:11.  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.  
 OS Homo sapiens.  
 XX JP2000080100-A.  
 XX 21-MAR-2000.  
 XX 12-OCT-1998; 98JP-0304793.  
 XX 17-JUN-1998; 98JP-0188196.  
 XX 26-JUN-1998; 98JP-0196729.  
 XX (NISR) JAPAN TOBACCO INC.  
 PA WPI; 2000-286723/25.  
 DR P-PSDB; AAY82614.  
 XX A human monoclonal antibody to parathyroid hormone related protein, -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain  
 XX Example 10; Page 41-42; 88pp; Japanese.  
 CC The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment  
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a  
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the  
 CC present invention.  
 SQ Sequence 720 BP; 174 A; 190 C; 188 G; 163 T; 5 other;  
 Query Match 83.2%; Score 599.4; DB 21; Length 720;  
 Best Local Similarity 89.4%; Pred. No. 4e-150;  
 Matches 642; Conservative 0; Mismatches 76; Indels 0; Gaps 0;  
 QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTCGCTCGGTCCTCGGGTCCAGTGGG 60  
 DB 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTCGCTCGGTCCTCGGGTCCAGTGGG 60  
 QY 61 GAAGTTGTGATGATCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGAGCCGGCTCC 120  
 DB 61 GATATTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
 QY 121 ATCTCTGTAGTGTAGTCAAGCCTTAAACACAGTAAATGGAGACACCTTCCTGAGTTGG 180  
 DB 121 ATCTCTGTAGTGTAGTCAAGCCTTAAACACAGTAAATGGAGACACCTTCCTGAGTTGG 180  
 QY 181 TATCAGCAGAGCCAGGCAACCTCCAGGCTCCTGATTTATTAAGGTTCTTAACCGGGAC 240  
 DB 181 TACCTGCAGAGCCAGGCAACCTCCAGGCTCCTGATTTATTAAGGTTCTTAACCGGGAC 240  
 QY 241 TCTGGGTTCCAGACAGATTTCAGGCGAGTGGGGAGGAGGACAGATTTCACACTGAAATTC 300  
 DB 241 TCTGGGTTCCAGACAGATTTCAGGCGAGTGGGGAGGAGGACAGATTTCACACTGAAATTC 300

Db 541 TCGGGTAACTCCAGGAGAGTGTCTACAGAGCAGGACGACACCTACAGCCTC 600  
 QY 601 AGCAGCACCTGAGCGTGAAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660  
 Db 601 AGCAGCACCTGAGCGTGAAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660  
 QY 661 GTACCCATCAGGGCCTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 718  
 Db 661 GTACCCATCAGGGCCTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 718

RESULT 13  
 ID AAA78267  
 XX AAA78267 standard; DNA; 720 BP.  
 XX AC AAA78267;  
 XX DT 16-NOV-2000 (first entry)  
 XX DE Anti-human Fas immunoglobulin M light chain DNA sequence SEQ ID #77.  
 XX KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
 XX KW immunosuppression; autoimmune disease; treatment; rheumatism;  
 XX KW anti-Fas antibody; ss.  
 XX OS Synthetic.  
 XX PN JP2000154149-A.  
 XX PD 06-JUN-2000.  
 XX PF 17-SEP-1999; 99JP-0263984.  
 XX PR 18-SEP-1998; 98JP-0264598.  
 XX PA (SANYO) SANKYO CO LTD.  
 XX DR WPI; 2000-454476/40.  
 XX DR P-PSDB; AAB12913.  
 XX PT Anti-human Fas humanizing antibody-containing antirheumatic agents -  
 XX PS Example 2; Page 65-66; 109pp; Japanese.  
 XX CC The present invention relates to antirheumatic agents which comprise as  
 CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
 CC does not include a J segment, has apoptosis inducing activity, and  
 CC consists of a light and heavy chain polypeptide produced synthetically.  
 CC The agents of the invention exhibit antirheumatic and immunosuppressive  
 CC activity and can be used to treat autoimmune diseases, especially  
 CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
 CC binding properties. Included in the invention are nucleotide sequences  
 CC of the IgM light and heavy chains (see AAA78267-A78272) and the  
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
 CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also  
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
 CC chains used in the invention are represented by sequences  
 CC AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AAA78277-A78318 and  
 CC AAA78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are  
 CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer  
 CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in  
 CC the production of the agent of the invention.

Seq Sequence 720 BP; 180 A; 200 C; 184 G; 156 T; 0 other;  
 Query Match 85.7%; Score 617.2; DB 21; Length 720;  
 Best Local Similarity 91.2%; Pred. No. 7.2e-155;  
 Matches 655; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTCGCTCCCGGTCAGTGGG 60  
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 QY 61 GAAGTTGTGATGACTCAGTCTCCACCTGCTCCCTTCCCATCACACCTTGAGAGCGGGCTCC 120  
 Db 61 GATTTGTGATGACTCAGTCTCCACCTGCTCCCTTCCCATCACACCTTGAGAGCGGGCTCC 120  
 QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACAGTAAAGAGACACCTTCTGAGTTGG 180  
 Db 121 ATCTCTGTAGTCTAGTCAAGCCTTAAAGAGCTTGTACACAGTAATGAAACACCTATTATCATTTG 180  
 QY 181 TATCAGCAGAGCAGGCGCCCAACCTCAAGGCTCTGATTTATAAGTTTCTAACCGGAC 240  
 Db 181 TACCTGCAGAGCAGGCGCCAGTCTCAAAAGCTCTGATCTACAAAGTTTCCAACCGATTT 240  
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 Db 241 TCTGGGGTCCCGACAGACAGATTTCAGCGGCGAGTTCAGGCACTGATTTTCACTGAAATC 300  
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 Db 301 AGCAGGTTGGAGGCTGAAGATGTTGGGTTTATTTCTCTCAAAGTACACATGTTCTCT 360  
 QY 361 CCCACTTTCCGCGGAGGACCAAGGTGGAAATCAAACTGACGTTGGCTGCACCATCTGTC 420  
 Db 361 CCGGCGTTCCGCGGCAAGGGACCAAGGTGGAAATCAAACTGACGTTGGCTGCACCATCTGTC 420  
 QY 421 TTCTATCTTCCCGCCCTCTGATGAGCAGTTTGAATCTGGAACTGCTGTTGTGTGCTG 480  
 Db 421 TTCTATCTTCCCGCCCTCTGATGAGCAGTTTGAATCTGGAACTGCTGTTGTGTGCTG 480  
 QY 481 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAA 540  
 Db 481 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAA 540  
 QY 541 TCGGGTAATCCCGAGGAGTGTCAAGAGCAGGACGAGCAGCAGCAGCAGCAGCAGCCTC 600  
 Db 541 TCGGGTAATCCCGAGGAGTGTCAAGAGCAGGACGAGCAGCAGCAGCAGCAGCAGCCTC 600  
 QY 601 AGCAGCACCTGAGCGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660  
 Db 601 AGCAGCACCTGAGCGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660  
 QY 661 GTACCCATCAGGGCCTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 718  
 Db 661 GTACCCATCAGGGCCTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 718

RESULT 14  
 ID AAF44895 standard; cDNA; 963 BP.  
 XX AAF44895;  
 XX AC AAF44895;  
 XX DT 28-MAR-2001 (first entry)  
 XX DE Human breast cancer related protein coding sequence SEQ ID NO: 51.  
 XX KW Human; breast cancer; diagnosis; therapy; vaccine; ss.  
 XX OS Homo sapiens.  
 XX PN WO200078960-A2.  
 XX PD 28-DEC-2000.  
 XX PF 23-JUN-2000; 2000WO-US17536.  
 XX PR 23-JUN-1999; 99US-0140903.  
 XX PR 12-OCT-1999; 99US-0158980.  
 XX PA (CORI-) CORIAX CORP.

```
QY 121 ATCTCTGTAGTCTAGTCAAAAGCCTTAAACACAGTAATGGAGACACCTTCTCGATTGG 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 ATCTCTGCAGATCTAGTAAGAGCCTTGTACACAGTAATGGAAACACCTATTACATTGG 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TATACAGACAAGCCAGGCCAACTCAAGGCTCCTGATTTATAAGGTTTCTAAACGGGAC 240
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TACTCTGAGAAGCCAGGCCAGTCTCAAGGCTCCTGATCTACAAAGTTTCCAACCGATT 240
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 TCTGGGGTCCACAGACAGATTACGGCAGTGGGCGAGGACAGATTTACACTGAAATC 300
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 301 AGCAGGTTGGAGGCTGAGGATGTTGGGGTTTATTTACTGCTCTCAAGTACACATGTTCT 360
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QY 361 CCCACTTTGGGGAGGAGACCAAGGTGGAATCAACGTACGGTGGCTGCACCATCTGTC 420
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QY 361 CCGGCGTTTCGGCCCAAGGACCAAGGTGGAATCAACGTACTGTGGCTGCACCATCTGTC 420
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QY 421 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGGAATCTGTTGTGCTG 480
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGTTGTGCTG 480
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGATAACGCCCTCCAA 540
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGATAACGCCCTCCAA 540
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 541 TCGGGTAATCTCCAGGAGAGTGTCAAGAGCAGGACAGCAAGGACAGCACTACAGCCTC 600
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 541 TCGGGTAATCTCCAGGAGAGTGTCAAGAGCAGGACAGCAAGGACAGCACTACAGCCTC 600
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 601 AGCAGCAGCCTGAGCTGAGCAAGCAGACTACGAGAACAAAGTCTACGAGTCTACGCGG 660
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 601 AGCAGCAGCCTGAGCTGAGCAAGCAGACTACGAGAACAAAGTCTACGAGTCTACGCGG 660
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 661 GTCAACCATCAGGGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 661 GTCAACCATCAGGGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
AAV61359
ID AAV61359 standard; cDNA to mRNA; 720 BP.
AC AAV61359;
AC AAV61359;
XX
XX
DT 18-JAN-1999 (first entry)
XX
DE Anti-human Fas humanised antibody CH11 light chain VL-KY cDNA.
XX
XX
KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
KW autoimmune disease; rheumatoid arthritis; therapy; human;
KW antibody engineering; ds.
XX
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT sig_peptide 1..60
FT /*tag= a
FT mat_peptide 61..717
FT /*tag= b
XX
XX
PN EP866131-A2.
XX
XX
PD 23-SEP-1998.
XX
XX
PF 20-MAR-1998; 98EP-0302113.
XX
XX
PR 21-MAR-1997; 97JP-0067938.
XX
XX
PA (SANTY ) SANKYO CO LTD.
```

```
XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;
PI Yonehara S;
XX WPI; 1998-482965/42.
DR P-PSDB; AAW71876.
XX Production of anti-Fas protein humanised antibodies - for use in
PT inducing apoptosis on Fas expressing cells in the treatment of
PT autoimmune diseases, especially rheumatoid arthritis
XX Example 3; Page 92-93; 187pp; English.
PS
XX This cDNA sequence codes for a humanised anti-Fas antibody CH11
CC light chain (see AAW71876), designated VL-KY. VL-KY is based on the
CC light chain (see AAW71889) of murine anti-human Fas monoclonal
CC antibody CH11. The humanised sequence was designed following
CC selection of donor residues from CH11 to be grafted onto acceptor
CC molecule RPM1610'CL. 4 Light chain sequences (see AAW71876-79) have
CC been designed, and each can be used in combination with either of 2
CC heavy chain sequences (see AAW71880-81) to provide novel, claimed
CC humanised CH11 IGM antibodies that lack a J chain. These humanised
CC anti-human Fas antibodies are capable of inducing apoptosis in cells
CC expressing Fas (e.g. synoviocytes) and are useful in the treatment
CC of autoimmune disease and chronic rheumatoid arthritis. DNA
CC sequences encoding the humanised antibodies are claimed, as are
CC vectors such as pKappakV2-58 including the VL-KY nucleotide
CC sequence, and host cells such as Escherichia coli pKappakV2-58
CC (FERM BP-5861).
XX
SQ Sequence 720 BP; 180 A; 200 C; 184 G; 156 T; 0 other;
```

```
Query Match 85.7%; Score 617.2; DB 19; Length 720;
Best Local Similarity 91.2%; Pred. No. 7.2e-155;
Matches 655; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 ATGAGCCTCCCTGCTGCTCAGCTCCTCGGCTCTATTGCTCTGCGTCCCGGTCCAGTGG 60
DB 1 ATGAGGCTCCCTGCTCAGCTCCTGGGCTGCTAATGCTCTGCGTCCCGGTCCAGTGG 60
QY 61 GAAGTTGTGATGACTGACTGCTCCACTGCTCCCTTCCCATCACACTGGAGAGCGGCTCC 120
DB 61 GATGTTGTGATGACTGACTGCTCCACTGCTCCCTTCCCATCACACTGGAGAGCGGCTCC 120
QY 121 ATCTCTGTAGTCTAGTCAAAAGCCTTAAACACAGTAATGGAGACACCTTCTCGATTGG 180
DB 121 ATCTCTGCAGATCTAGTAAGAGCCTTGTACAGTAATGGAAACACCTATTACATTGG 180
QY 181 TATCAGCAGAAGCCAGGCCAACTCCAAAGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240
DB 181 TACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGGATT 240
QY 241 TCTGGGTCCACAGACAGATTACGGCGCAGTGGGCGAGGACAGATTTACACTGAAATC 300
DB 241 TCTGGGTCCACAGACAGATTACGGCGCAGTGGGTCAGGCACTGATTTACACTGAAATC 300
QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGCAAGGTACAAAGACTCCT 360
DB 301 AGCAGGTTGGAGGCTGAGGATGTTGGGGTTTATTTACTGCTCTCAAGTACACATGTTCT 360
QY 361 CCCACTTTTCGGCGGAGGACCAAGGTGGAATCAACGTACGGTGGCTGCACCATCTGTC 420
DB 361 CCGGCGTTTCGGCCCAAGGACCAAGGTGGAATCAACGTACTGTGGCTGCACCATCTGTC 420
QY 421 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCTGTTGTGCTGCTG 480
DB 421 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCTGTTGTGCTGCTG 480
QY 481 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGATAACGCCCTCCAA 540
DB 481 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGATAACGCCCTCCAA 540
QY 541 TCGGGTAATCTCCAGGAGAGTGTCAAGAGCAGGACAGCAAGGACAGCACTACAGCCTC 600
```

CC The present invention relates to antirheumatic agents which comprise as  
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
CC does not include a J segment, has apoptosis inducing activity, and  
CC consists of a light and heavy chain polypeptide produced synthetically.  
CC The agents of the invention exhibit antirheumatic and immunosuppressive  
CC activity and can be used to treat autoimmune diseases, especially  
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
CC binding properties. Included in the invention are nucleotide sequences  
CC of the IgM light and heavy chains (see AAB12902-B12907) and the  
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
CC AAB12902-A78206) and protein sequences (see AAB12908-B12910). Also  
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
CC chains used in the invention are represented by sequences  
CC AAB12913-A78266. Primers used for sequencing the human Ig DNA used in the  
CC invention are represented by sequences AAB12913-A78266 and  
CC AAB12913-A78337, while humanised anti-Fas Ig DNA sequencing primers are  
CC represented by sequences AAB12913-A78334 and AAB12913-A78367. Primer  
CC sequences AAB12907-A78212 are specific for murine Ig DNA, and are used in  
CC the production of the agent of the invention.

XX SQ Sequence 720 BP; 179 A; 200 C; 184 G; 157 T; 0 other;

Query Match 85.9%; Score 618.8; DB 21; Length 720;  
Best Local Similarity 91.4%; Pred. No. 2.7e-155;  
Matches 656; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCCCTGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60  
DB 1 ATGAGGCTCCCTGCTCAGCTCCCTGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60  
QY 61 GAAGTTGTGATGACTCAGTCTCAGTCTCCACTTCCCTGCTCCCGTCCAGCAGCGGCTCC 120  
DB 61 GATGTTGTGATGACTCAGTCTCAGTCTCCACTTCCCTGCTCCCGTCCAGCAGCGGCTCC 120  
QY 121 ATCTCCTGTAGTCTAGTCAAGCTTAAACAGAGTAATGAGACACCTTCCTGAGTGG 180  
DB 121 ATCTCCTGTAGTCTAGTCAAGCTTAAACAGAGTAATGAGACACCTTCCTGAGTGG 180  
QY 181 TATCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
DB 181 TACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
QY 241 TCTGGGTTCCAGACAGATTTCAGGCGGAGTGGGCGAGGAGGAGGAGGAGGAGGAGGAG 300  
DB 241 TCTGGGTTCCAGACAGATTTCAGGCGGAGTGGGCGAGGAGGAGGAGGAGGAGGAGGAG 300  
QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGTTTATTTCTGCGGGCAAGGTACAGGACTCCT 360  
DB 301 AGCAGGTGGAGGCTGAGGATGTTGGGTTTATTTCTGCTCTCAAGTACACATGTTCTCT 360  
QY 361 CCCATTTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
DB 361 CCGGCGTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
QY 421 TCACTCTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
DB 421 TCACTCTTCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
QY 481 CTGAATTAACCTTCTATCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
DB 481 CTGAATTAACCTTCTATCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
QY 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
DB 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
QY 601 AGCAGACCTCTGACGTTGAGCAAGAGGAGTACGAGAGGAGGAGGAGGAGGAGGAGGAG 660  
DB 601 AGCAGACCTCTGACGTTGAGCAAGAGGAGTACGAGAGGAGGAGGAGGAGGAGGAGGAG 660  
QY 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAGAGCTTCAACAGGAGGAGGAGTGT 718

DB 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAGAGCTTCAACAGGAGGAGTGT 718

## RESULT 11

AAA78269  
ID AAA78269 standard; DNA; 720 BP.  
XX AAA78269;  
AC AAA78269;  
XX 16-NOV-2000 (first entry)

DE Anti-human Fas immunoglobulin M light chain DNA sequence SEQ ID #81.  
KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
KW immunosuppression; autoimmune disease; treatment; rheumatism;  
KW anti-Fas antibody; ss.  
OS Synthetic.

PN JP2000154149-A.

XX 06-JUN-2000.

XX 17-SEP-1999; 99JP-0263984.

XX 18-SEP-1998; 98JP-0264598.

XX (SANY ) SANKYO CO LTD.

XX WPI; 2000-454476/40.

XX P-PSDB; AAB12915.

XX Anti-human Fas humanizing antibody-containing antirheumatic agents -

XX Example 2; Page 69-70; 109pp; Japanese.

CC The present invention relates to antirheumatic agents which comprise as  
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
CC does not include a J segment, has apoptosis inducing activity, and  
CC consists of a light and heavy chain polypeptide produced synthetically.  
CC The agents of the invention exhibit antirheumatic and immunosuppressive  
CC activity and can be used to treat autoimmune diseases, especially  
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
CC binding properties. Included in the invention are nucleotide sequences  
CC of the IgM light and heavy chains (see AAB12913-B12918 and AAB12919), and  
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
CC AAB12902-A78206) and protein sequences (see AAB12908-B12910). Also  
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
CC chains used in the invention are represented by sequences  
CC AAB12913-A78266. Primers used for sequencing the human Ig DNA used in the  
CC invention are represented by sequences AAB12913-A78266 and  
CC AAB12913-A78337, while humanised anti-Fas Ig DNA sequencing primers are  
CC represented by sequences AAB12913-A78334 and AAB12913-A78367. Primer  
CC sequences AAB12907-A78212 are specific for murine Ig DNA, and are used in  
CC the production of the agent of the invention.

XX SQ Sequence 720 BP; 179 A; 200 C; 185 G; 156 T; 0 other;

Query Match 85.9%; Score 618.8; DB 21; Length 720;  
Best Local Similarity 91.4%; Pred. No. 2.7e-155;  
Matches 656; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGCTCCCTGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60

DB 1 ATGAGGCTCCCTGCTCAGCTCCCTGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60

QY 61 GAAGTTGTGATGACTCAGTCTCAGTCTCCACTTCCCTGCTCCCATCACACTGGAGAGCGGCTCC 120

DB 61 GATGTTGTGATGACTCAGTCTCAGTCTCCACTTCCCTGCTCCCATCACACTGGAGAGCGGCTCC 120

AC AAV61361;  
 XX  
 DT 18-JAN-1999 (first entry)  
 XX  
 DE Anti-human Fas humanised antibody CH11 light chain VL-RY cDNA.  
 XX  
 XX Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;  
 KW autoimmune disease; rheumatoid arthritis; therapy; human;  
 KW antibody engineering; ds.  
 XX  
 KW Homo sapiens.  
 OS Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH sig\_peptide 1..60  
 FT /tag= a  
 FT mat\_peptide 61..717  
 FT /tag= b  
 FT  
 XX  
 PN EP866131-A2.  
 XX  
 XX 23-SEP-1998.  
 PD  
 XX  
 PF 20-MAR-1998; 98EP-0302113.  
 PR  
 PR 21-MAR-1997; 97JP-0067938.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 PA  
 XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;  
 PI Yonehara S;  
 PI  
 XX  
 DR WPI; 1998-482965/42.  
 DR P-PSDB; AAW71878.  
 XX  
 XX  
 PT Production of anti-Fas protein humanised antibodies - for use in  
 PT inducing apoptosis on Fas expressing cells in the treatment of  
 PT autoimmune diseases, especially rheumatoid arthritis  
 XX  
 PS Example 3; Page 97-98; 187pp; English.  
 XX  
 CC This cDNA sequence codes for a humanised anti-Fas antibody CH11  
 CC light chain (see AAW71878), designated VL-RY. VL-RY is based on the  
 CC light chain (see AAW71889) of murine anti-human Fas monoclonal  
 CC antibody CH11. The humanised sequence was designed following  
 CC selection of donor residues from CH11 to be grafted onto acceptor  
 CC molecule RPMI6410'CL. 4 Light chain sequences (see AAW71876-79) have  
 CC been designed, and each can be used in combination with either of 2  
 CC heavy chain sequences (see AAW71880-81) to provide novel, claimed  
 CC humanised CH11 IgM antibodies that lack a J chain. These humanised  
 CC anti-human Fas antibodies are capable of inducing apoptosis in cells  
 CC expressing Fas (e.g. synovocytes) and are useful in the treatment  
 CC of autoimmune disease and chronic rheumatoid arthritis. DNA  
 CC sequences encoding the humanised antibodies are claimed, as are  
 CC vectors such as pPKkappRY2-10 including the VL-RY nucleotide  
 CC sequence, and host cells such as Escherichia coli pKkappRY2-10  
 CC (PERM BP-5859).  
 XX  
 SQ Sequence 720 BP; 179 A; 200 C; 185 G; 156 T; 0 other;

Query Match 85.9%; Score 618.8; DB 19; Length 720;  
 Best Local Similarity 91.4%; Pred. No. 2.7e-155;  
 Matches 656; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 ATGAGGCTCCCTCAGCTCCCTGGGCTGCTATTGCTGCTCCCGGCTCCAGTGGG 60  
 DB |||||  
 QY 1 ATGAGGCTCCCTCAGCTCCCTGGGCTGCTATTGCTGCTCCCGGCTCCAGTGGG 60  
 DB |||||  
 QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCCACTCGAGCGGGCTCC 120  
 DB |||||  
 QY 61 GATGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCGTCCAGTGGACAGCGGCTCC 120  
 DB |||||  
 QY 121 ATCTCCTGTAGGCTAGTCAAGGCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG 180  
 XX |||||

Db 121 ATCTCCTGCAGATCTAGTAAAGGCTTGTACAGTAATGGAACACCTATTATCATGG 180  
 QY |||||  
 QY 181 TATCAGCAGAAAGCCAGGCCAACCTTCAAGGCTCTGATTTATTAAGGTTTCTTAACCGGAC 240  
 Db |||||  
 Db 181 TACCTGCAGAAAGCCAGGCCAGCTCTCAAGGCTCTGATCTACAAAGTTTCCACCGGATTT 240  
 QY |||||  
 QY 241 TCTGGGTCTCCAGACAGATTCAGGGCAGTGGGCGGACAGATTTACACACTGAAATC 300  
 Db |||||  
 Db 241 TCTGGGTCTCCAGACAGATTCAGGGCAGTGGGCTGAGTTTCACACTGAAATC 300  
 QY |||||  
 QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGCTTTATTTCTGCGGGCAAGGTACAAGGACTCCT 360  
 Db |||||  
 Db 301 AGCAGGTGGAGGCTGAGGATGTTGGGCTTTATTTCTGCTCTCAAAGTACACATGTTCT 360  
 QY |||||  
 QY 361 CCCACTTTTCGGCGGAGGACCAAGGTGGAATCAAAAGTACGGTGGTGCACCACTCTGTC 420  
 Db |||||  
 Db 361 CCGGCGTTTCGGCCCAAGGACCAAGGTGGAATCAAAAGTACTGTGGCTGCACCATCTGTC 420  
 QY |||||  
 QY 421 TTCACTTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTG 480  
 Db |||||  
 Db 421 TTCACTTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTG 480  
 QY |||||  
 QY 481 CTGAATAACTTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAA 540  
 Db |||||  
 Db 481 CTGAATAACTTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAA 540  
 QY |||||  
 QY 541 TCGGGTAATCCAGAGAGTGTCTACAGAGCAGACAGCAGAGCAGCAGCTACAGGCTC 600  
 Db |||||  
 Db 541 TCGGGTAATCCAGAGAGTGTCTACAGAGCAGACAGCAGAGCAGCAGCTACAGGCTC 600  
 QY |||||  
 QY 601 AGCAGACCCCTGACGCTGAGCAAGAGCAGCTACGAGAAACACAAAGTCTACGCTCGGAA 660  
 Db |||||  
 Db 601 AGCAGACCCCTGACGCTGAGCAAGAGCAGCTACGAGAAACACAAAGTCTACGCTCGGAA 660  
 QY |||||  
 QY 661 GTCACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGAGAGTGT 718  
 Db |||||  
 Db 661 GTCACCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGAGAGTGT 718

RESULT 10  
 AAA78268  
 ID AAA78268 standard; DNA; 720 BP.  
 AC AAA78268;  
 XX  
 DT 16-NOV-2000 (first entry)  
 XX  
 DE Anti-human Fas immunoglobulin M light chain DNA sequence SEQ ID #79.  
 XX  
 KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
 KW immunosuppression; autoimmune disease; treatment; rheumatism;  
 XX anti-Fas antibody; ss.  
 XX Synthetic.  
 OS  
 XX JP2000154149-A.  
 PN  
 PD 06-JUN-2000.  
 XX  
 PF 17-SEP-1999; 99JP-0263984.  
 XX  
 PR 18-SEP-1998; 98JP-0264598.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 PA  
 XX WPI; 2000-454476/40.  
 DR P-PSDB; AAB12914.  
 XX  
 PT Anti-human Fas humanizing antibody-containing antirheumatic agents -  
 PS Example 2; Page 67-68; 109pp; Japanese.  
 XX

QY 361 CCACATTTTCGGCGGAGGACCAAGGTGGAAATCAAAAGTACGGTGGCTGCACCATCTGTC 420  
DB 401 TGGACGCTTCGGCCCAAGGAGCGAAGGTGGAAACCAAAACGAAGTGTGGCTGCACCATCTGTC 460  
QY 421 TTCAATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTCTTGTGTGCGCTG 480  
DB 461 TTCAATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTCTTGTGTGCGCTG 520  
QY 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATTAACGCCCTCCAA 540  
DB 521 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATTAACGCCCTCCAA 580  
QY 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGACAGACCTACAGCCTC 600  
DB 581 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGACAGACCTACAGCCTC 640  
QY 601 AGCAGACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAA 660  
DB 641 AGCAGACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAA 700  
QY 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCCACAAAGAGCTTCAACAGGGGAGAGTGT 718  
DB 701 GTCAACCATCAGGCGCTGAGCTCGCCCGTCCACAAAGAGCTTCAACAGGGGAGAGTGT 758

RESULT 8  
AAV61360  
ID AAV61360 standard; cDNA to mRNA; 720 BP.

AC AAV61360;  
XX  
DT 18-JAN-1999 (first entry)  
XX  
DE Anti-human Fas humanised antibody CH11 light chain VL-KF cDNA.  
XX  
KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;  
KW autoimmune disease; rheumatoid arthritis; therapy; human;  
KW antibody engineering; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT sig\_peptide 1..60  
FT /\*tag= a  
FT mat\_peptide 61..717  
FT /\*tag= b  
XX  
EP866131-A2.  
XX  
PD 23-SEP-1998.  
XX  
PF 20-MAR-1998; 98EP-0302113.  
XX  
PR 21-MAR-1997; 97JP-0067938.  
XX  
(SANY ) SANKYO CO LTD.  
XX  
PI Haruyama H, Nakahara K, Serizawa N, Takahashi T;  
PI Yonehara S;  
XX  
XX  
DR WPI; 1998-482965/42.  
DR P-PSDB; AAW71877.  
XX  
XX  
PT Production of anti-Fas protein humanised antibodies - for use in  
PT inducing apoptosis on Fas expressing cells in the treatment of  
PT autoimmune diseases, especially rheumatoid arthritis  
XX  
PS Example 3; Page 95-96; 187pp; English.  
XX  
XX

CC This cDNA sequence codes for a humanised anti-Fas antibody CH11  
CC light chain (see AAW71877), designated VL-KF. VL-KF is based on the  
CC light chain (see AAW71889) of murine anti-human Fas monoclonal

CC antibody CH11. The humanised sequence was designed following  
CC selection of donor residues from CH11 to be grafted onto acceptor  
CC molecule RPI6410'CL. 4 Light chain sequences (see AAW71876-79) have  
CC been designed, and each can be used in combination with either of 2  
CC heavy chain sequences (see AAW71880-81) to provide novel, claimed  
CC humanised CH11 IGM antibodies that lack a J chain. These humanised  
CC anti-human Fas antibodies are capable of inducing apoptosis in cells  
CC expressing Fas (e.g. synovocytes) and are useful in the treatment  
CC of autoimmune disease and chronic rheumatoid arthritis. DNA  
CC sequences encoding the humanised antibodies are claimed, as are  
CC vectors such as pKappaK2-19 including the VL-KF nucleotide  
CC sequence, and host cells such as Escherichia coli pKappaK2-19  
CC (FERM BP-5860).  
XX  
SQ Sequence 720 BP; 179 A; 200 C; 184 G; 157 T; 0 other;

Query Match 85.9%; Score 618.8; DB 19; Length 720;  
Best Local Similarity 91.4%; Pred. No. 2.7e-155;  
Matches 656; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCTGCTCAGCTCCTCGGCTGCTATTTGCTCTCGCTCCCGGTCAGTGGG 60  
DB 1 ATGAGCCTCCTGCTCAGCTCCTCGGCTGCTATTTGCTCTCGCTCCCGGTCAGTGGG 60  
QY 61 GAAGTTGTGATGACTCAGTCTCCACTGCTCCCTCCCATCACACTGAGAGCGGCTCC 120  
DB 61 GATGTTGTGATGACTCAGTCTCCACTGCTCCCTCCCATCACACTGAGAGCGGCTCC 120  
QY 121 ATCTCTGTAGTCTAGTCAAGGCTTTAAACACAGTAACTGAGACACCTTCTCTGAGTTGG 180  
DB 121 ATCTCTGTAGTCTAGTCAAGGCTTTAAACACAGTAACTGAGACACCTTCTCTGAGTTGG 180  
QY 181 TATCAGCAGAAAGCCAGGCCAACCTCCAAAGCTCTCTGATTTATTAAGGTTTCTAACCGGAC 240  
DB 181 TACCTGAGAAAGCCAGGCCAGTCTCTCAAGCTCTCTGATCTACAAAGTTTCCAAACCGATT 240  
QY 241 TCTGGGTCCTCAGACAGATTCAGCGGCGAGTGGGCGAGGACAGATTTACACATGAAATC 300  
DB 241 TCTGGGTCCTCAGACAGATTCAGCGGCGAGTGGGCGAGGACAGATTTACACATGAAATC 300  
QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTCGGGCAAGGTACAGGACTCCT 360  
DB 301 AGCGGCTGGAGGCTGAGGATGTTGGGGTTTATTTCTCTCTCAAGTACACATGTTCTCT 360  
QY 361 CCCACTTTTCGGCGGAGGACCAAGTGGAAATCAAAAGTACGCTGCTGACCAATCTGTC 420  
DB 361 CCGGCTTCGGGCCAAGGACCAAGTGGAAATCAAAAGTACGCTGCTGCTGACCAATCTGTC 420  
QY 421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTGTGCTG 480  
DB 421 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTGTGCTG 480  
QY 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATTAACGCCCTCCAA 540  
DB 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATTAACGCCCTCCAA 540  
QY 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600  
DB 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600  
QY 601 AGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAA 660  
DB 601 AGCAGCACCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAA 660  
QY 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCCACAAAGAGCTTCAACAGGGGAGAGTGT 718  
DB 661 GTCAACCATCAGGCGCTGAGCTCGCCCGTCCACAAAGAGCTTCAACAGGGGAGAGTGT 718

RESULT 9  
AAV61361  
ID AAV61361 standard; cDNA to mRNA; 720 BP.  
XX

CC antibodies comprising humanised light and heavy chains (see  
CC AAW71876-81) derived from the murine anti-human Fas monoclonal  
CC antibody CH11. The humanised anti-human Fas antibodies are  
CC capable of inducing apoptosis in cells expressing Fas (e.g.  
CC synovialocytes) and are useful in the treatment of autoimmune disease  
CC and chronic rheumatoid arthritis.  
XX  
SQ Sequence 891 BP; 204 A; 267 C; 225 G; 195 T; 0 other;  
  
Query Match 86.2%; Score 620.4; DB 19; Length 891;  
Best Local Similarity 91.5%; Pred. No. 1.1e-155;  
Matches 657; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
  
QY 1 ATGAGCCTCCCTGCTCAGCTCTCGGGCTGCTATTGCTCTGGTCCCGGGTCCAGTGGG 60  
Db |||||  
QY 41 ATGAGCCTCCCTGCTCAGCTCTCGGGCTGCTATTGCTCTGGTCCAGGATCCAGTGGG 100  
Db |||||  
QY 61 GAAGTTGTGATGATCTCAGTCTCCAGTCTCCCTTCCCATCACACCTGGAGAGCGGCTCC 120  
Db |||||  
QY 101 GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACTCCCTGGACAGCGGCTCC 160  
Db |||||  
QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGGAGACACCTTCTGAGTTGG 180  
Db |||||  
QY 161 ATCTCTGCTGAGCTCTAGTCAAGCCTCTGTTTTCAGTGATGGAACACCTACGTGAATTGG 220  
Db |||||  
QY 181 TATCAGCAGAACCGGCGCAACTCCAGGCTCTGATTATTAAGTTTCTAAACCGGAC 240  
Db |||||  
QY 221 TTTTCATCAGAGGCCAGGCGCAACTCCAGGCGCTAAATTTATGAGTTTCTCACGGGAC 280  
Db |||||  
QY 241 TCTGGGTCCTCCAGACAGATTCAGCGGCTGAGTGGGCGGAGGACAGATTTCACTGAAATC 300  
Db |||||  
QY 281 TCTGGGTCCTCCAGACAGATTCAGCGGCGGAGTGGGTGAGGCTGATTTTCACACTGAAATC 340  
Db |||||  
QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGGGCGAAGGTACAGGACTCCT 360  
Db |||||  
QY 341 AGCAGGGTGGAGGCTGAGGATGTTGGGGTTTATTTACTGATGCAAGGTACAGTGGCGG 400  
Db |||||  
QY 361 CCCACTTTTCGGCGGAGGACCAAGGTGGAATCAAACTGACGGTGGCTGCACCATCTGTC 420  
Db |||||  
QY 401 TGGAGCTTCGGCGCAAGGACGAAAGTGGAAACCAACGAACTGTGGCTGCACCATCTGTC 460  
Db |||||  
QY 421 TTTCATCTTCCCGCCACTCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGGCTG 480  
Db |||||  
QY 461 TTTCATCTTCCCGCCACTCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGGCTG 520  
Db |||||  
QY 481 CTGAATACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAAGCGCCCTCAA 540  
Db |||||  
QY 521 CTGAATACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAAGCGCCCTCAA 580  
Db |||||  
QY 541 TCGGGTAATCTCCAGGAGAGTGTACAGAGCAGACAGCAGCAGCAGCAGCAGCAGCAGC 600  
Db |||||  
QY 581 TCGGGTAATCTCCAGGAGAGTGTACAGAGCAGACAGCAGCAGCAGCAGCAGCAGCAGC 640  
Db |||||  
QY 601 AGCAGCAGCCTGACGCTGAGCAAGACAGCTACAGAGAAACACAAAGTCTAGCGCTCGAA 660  
Db |||||  
QY 641 AGCAGCAGCCTGAGCTGAGCAAGACAGCTACAGAGAAACACAACTCTAGCGCTCGAA 700  
Db |||||  
QY 661 GTCAACCATCAGGCGCTGAGCTCGCGCTGACAAAGAGCTTCAACAGGGAGAGTGT 718  
Db |||||  
QY 701 GTCAACCATCAGGCGCTGAGCTCGCGCTGACAAAGAGCTTCAACAGGGAGAGTGT 758  
Db |||||  
  
RESULT 7  
AAW78320  
ID AAA78320 standard; DNA; 891 BP.  
XX  
AC AAA78320;  
XX  
XX  
DT 16-NOV-2000 (first entry)  
XX  
DE Anti-human Fas Ig CH11 nucleotide SEQ ID #138.  
XX  
XX Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;

KW immunosuppression; autoimmune disease; treatment; rheumatism;  
KW anti-Fas antibody; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2000154149-A.  
XX  
XX 06-JUN-2000.  
XX  
XX 17-SEP-1999; 99JP-0263984.  
XX  
XX 18-SEP-1998; 98JP-0264598.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX WPI; 2000-454476/40.  
XX  
XX Anti-human Fas humanizing antibody-containing antirheumatic agents -  
XX  
XX Example 5; Page 92; 109pp; Japanese.  
XX  
CC The present invention relates to antirheumatic agents which comprise as  
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
CC does not include a J segment, has apoptosis inducing activity, and  
CC consists of a light and heavy chain polypeptide produced synthetically.  
CC The agents of the invention exhibit antirheumatic and immunosuppressive  
CC activity and can be used to treat autoimmune diseases, especially  
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
CC binding properties. Included in the invention are nucleotide sequences  
CC of the IgM light and heavy chains (see AAW78267-A78272) and the  
CC corresponding protein sequences (see AAW12913-B12918 and AAW12919), and  
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
CC AAW78202-A78206) and protein sequences (see AAW12908-B12910). Also  
CC included are anti-human Fas antibody CDR peptides (AAW12902-B12907).  
CC Primers specific for the anti-human Fas antibody CDR peptides (AAW12902-B12907).  
CC chains used in the invention are represented by sequences  
CC AAW78213-A78266. Primers used for sequencing the human Ig DNA used in the  
CC invention are represented by sequences AAW78277-A78318 and  
CC AAW78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are  
CC represented by sequences AAW78321-A78334 and AAW78338-A78367. Primer  
CC sequences AAW78207-A78212 are specific for murine Ig DNA, and are used in  
CC the production of the agent of the invention.  
XX  
SQ Sequence 891 BP; 204 A; 267 C; 225 G; 195 T; 0 other;  
  
Query Match 86.2%; Score 620.4; DB 21; Length 891;  
Best Local Similarity 91.5%; Pred. No. 1.1e-155;  
Matches 657; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
  
QY 1 ATGAGCCTCCCTGCTCAGCTCTCGGGCTGCTATTGCTCTGGTCCCGGGTCCAGTGGG 60  
Db |||||  
QY 41 ATGAGCCTCCCTGCTCAGCTCTCGGGCTGCTATTGCTCTGGTCCCGGGTCCAGTGGG 100  
Db |||||  
QY 61 GAAGTTGTGATGATCTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGAGCGGCTCC 120  
Db |||||  
QY 101 GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACTCCCTGGACAGCGGCTCC 160  
Db |||||  
QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAAATGGAGACACCTTCTGAGTTGG 180  
Db |||||  
QY 161 ATCTCTGCTGAGCTCTAGTCAAGGCTCTGTTTTCAGTGATGGAACACCTACGTGAATTGG 220  
Db |||||  
QY 181 TATCAGCAGAACCGGCGCAACTCCAGGCTCTGATTATTAAGTTTCTAAACCGGAC 240  
Db |||||  
QY 221 TTTTCATCAGAGGCCAGGCGCAACTCCAGGCGCTAAATTTATGAGTTTCTCACGGGAC 280  
Db |||||  
QY 241 TCTGGGTCCTCCAGACAGATTCAGCGGCTGAGTGGGCGGAGGACAGATTTCACTGAAATC 300  
Db |||||  
QY 281 TCTGGGTCCTCCAGACAGATTCAGCGGCGGAGTGGGTGAGGCTGATTTTCACACTGAAATC 340  
Db |||||  
QY 301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGGGCGAAGGTACAGGACTCCT 360  
Db |||||  
QY 341 AGCAGGGTGGAGGCTGAGGATGTTGGGGTTTATTTACTGATGCAAGGTACAGTGGCGG 400  
Db |||||

XX  
DT 16-NOV-2000 (first entry)  
DE  
DE Anti-human Fas immunoglobulin M light chain DNA sequence SEQ ID #83.  
XX  
XX Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
KW immunosuppression; autoimmune disease; treatment; rheumatism;  
KW anti-Fas antibody; ss.  
XX  
XX Synthetic.  
OS  
OS JP2000154149-A.  
PN  
PN 06-JUN-2000.  
XX  
XX 17-SEP-1999; 99JP-0263984.  
PF  
XX 18-SEP-1998; 98JP-0264598.  
PR  
XX (SANY ) SANKYO CO LTD.  
PA  
XX WPI; 2000-454476/40.  
DR P-FSDB; AAB12916.  
XX  
XX Anti-human Fas humanizing antibody-containing antirheumatic agents -  
PT Example 2; Page 71-72; 109pp; Japanese.  
PS  
XX The present invention relates to antirheumatic agents which comprise as  
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
CC does not include a J segment, has apoptosis inducing activity, and  
CC consists of a light and heavy chain polypeptide produced synthetically.  
CC The agents of the invention exhibit antirheumatic and immunosuppressive  
CC activity and can be used to treat autoimmune diseases, especially  
CC rheumatism. The IgM molecule used in the invention are nucleotide sequences  
CC binding properties. Included in the invention are nucleotide sequences  
CC of the IgM light and heavy chains (see AAB12913-B12918 and AAB12919), and  
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
CC AAB12920-A78206) and protein sequences (see AAB12908-B12910). Also  
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
CC chains used in the invention are represented by sequences  
CC AAB12913-A78266. Primers used for sequencing the human Ig DNA used in the  
CC invention are represented by sequences AAB12918 and AAB12919.  
CC AAB12935-A78337, while humanised anti-Fas Ig DNA sequencing primers are  
CC represented by sequences AAB12921-A78334 and AAB12938-A78367. Primer  
CC sequences AAB12907-A78212 are specific for murine Ig DNA, and are used in  
CC the production of the agent of the invention.  
XX  
SQ Sequence 720 BP; 177 A; 200 C; 186 G; 157 T; 0 other;

Query Match 86.4%; Score 622; DB 21; Length 720;  
Best Local Similarity 91.6%; Pred. No. 3.8e-156;  
Matches 658; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGAGCTCCCTGCTCAGCTCCTGGGCTGCTATTGCTGCTGCTCCCGGTCAGTGGG 60  
Db |||||  
QY 1 ATGAGCTCCCTGCTCAGCTCCTGGGCTGCTATTGCTGCTGCTCCCGGTCAGTGGG 60  
Db |||||  
QY 61 GAAGTTGTGATGACTCAGTCTCCATCTGCTCCCTTCCCATCAGCTGGAGCCGGCTCC 120  
Db |||||  
QY 61 GATGTTGTGATGACTCAGTCTCCATCTGCTCCCTTCCCATCAGCTGGAGCCGGCTCC 120  
Db |||||  
QY 121 ATCTCTGTAGTCTAGTCAAGCTTAAACACAGTAAATGAGACACCTTCTCAGTTGG 180  
Db |||||  
QY 121 ATCTCTGTAGTCTAGTCAAGCTTAAACACAGTAAATGAGACACCTTCTCAGTTGG 180  
Db |||||  
QY 181 TATCAGCAGAGCCAGGCCAACCTTCAAGGCTCTGATTATTAAGGTTCTTAACCGGGAC 240  
Db |||||  
QY 181 TACCTCAGAGCCAGGCCAGCTCCAGGCTCTGATCTCAAAAGTTTCCACCGGATTT 240  
Db |||||  
QY 241 TCTGGGGTCCACAGATTCACGGCAGTGGGGGAGGAGGAGATTCACACTGAATC 300  
Db |||||

Db 241 TCTGGGGTCCACAGACAGATTGAGGGGAGTGGGTGAGGCACTGATTTCAACACGAAATC 300  
QY 301 AGCGCAGTGGAGGCTGAAAGATCTTGGGGTTTATTTCTCGCGGCAAGGTACAAGGACTCCT 360  
Db |||||  
Db 301 AGCAGGGTGGAGGCTGAGGATGTTGGGGTTTATTTCTGCTCTCAAGTACACATGTTCT 360  
QY 361 CCCATTCTTGGGGGAGGAGCAAGGTGGAATCAAGCTAGCGTGGCTGACCATCTGTC 420  
Db |||||  
Db 361 CCGGGCTTGGGCAAGGAGCAAGGTGGAATCAAGCTAGCTGTTGGCTGACCATCTGTC 420  
QY 421 TTCACTCTTCCGCCCATCTGATGAGCAGTTGAAATCTGAACTGCTCTGTTGTGCTG 480  
Db |||||  
Db 421 TTCACTCTTCCGCCCATCTGATGAGCAGTTGAAATCTGAACTGCTCTGTTGTGCTG 480  
QY 481 CTGAATAACTTCTATCCAGAGAGGCCAAGTACAGTGGAGTGGATTAAGCCCTCCAA 540  
Db |||||  
Db 481 CTGAATAACTTCTATCCAGAGAGGCCAAGTACAGTGGAGTGGATTAAGCCCTCCAA 540  
QY 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGGACAGGACACCTACAGCTC 600  
Db |||||  
Db 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGGACAGGACACCTACAGCTC 600  
QY 601 AGCAGCACCTGAGCGCTGAGCAAGAGAGCTACGAGAAACACAAAGTCTACGCTGCGAA 660  
Db |||||  
Db 601 AGCAGCACCTGAGCGCTGAGCAAGAGAGCTACGAGAAACACAAAGTCTACGCTGCGAA 660  
QY 661 GTCACCCATCAGGGGCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718  
Db |||||  
Db 661 GTCACCCATCAGGGGCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718

RESULT 6  
AAV66632  
ID AAV66632 standard; cDNA to mRNA; 891 BP.  
XX  
AC AAV66632;  
XX  
DT 18-JAN-1999 (first entry)  
XX  
DE Human immunoglobulin light chain cDNA.  
XX  
KW Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;  
KW autoimmune disease; rheumatoid arthritis; therapy; human;  
KW antibody engineering; ds.  
OS Homo sapiens.  
XX  
XX EP866131-A2.  
XX  
XX 23-SEP-1998.  
XX  
XX 20-MAR-1998; 98EP-0302113.  
XX  
XX 21-MAR-1997; 97JP-0057938.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX Hanyama H, Nakahara K, Serizawa N, Takahashi T;  
PI Yonehara S;  
XX  
XX WPI; 1998-482965/42.  
XX  
PT Production of anti-Fas protein humanised antibodies - for use in  
PT inducing apoptosis on Fas expressing cells in the treatment of  
PT autoimmune diseases, especially rheumatoid arthritis  
XX  
XX Example 4; Page 134; 187pp; English.  
XX  
CC This is the nucleotide sequence of the DNA insert of plasmid  
CC pHL 15-27 encoding human immunoglobulin light chain (subgroup II).  
CC It was obtained from human lymphocyte cDNA by PCR amplification  
CC (see also AAV61367-68). The invention relates to novel humanised



Db 361 CCCACTTTCGGCGGAGCACCAAGGTGGAATCAAAAGCTACGGTGGCTGCACCATCTGTC 420  
Qy 421 TTCAATCTCCCGCCATCTGATGAGCAGTGAATCTGGAATCTGGAATCTGCTGTTGTTGTCCTG 480  
Db 421 TTCAATCTCCCGCCATCTGATGAGCAGTGAATCTGGAATCTGGAATCTGCTGTTGTTGTCCTG 480  
Qy 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATACGCGCTCCAA 540  
Db 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATACGCGCTCCAA 540  
Qy 541 TCGGGTAATCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600  
Db 541 TCGGGTAATCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600  
Qy 601 AGCAGCACCTCTGAGCTGACCAAGCAGACTACGAGAACACAAAGTCTACGCTCGAA 660  
Db 601 AGCAGCACCTCTGAGCTGACCAAGCAGACTACGAGAACACAAAGTCTACGCTCGAA 660  
Qy 661 GTCAACCATCAGGCGCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGAGAGTGTGCA 720  
Db 661 GTCAACCATCAGGCGCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGAGAGTGTGCA 720

RESULT 4  
AAV61362  
ID AAV61362 standard; cDNA to mRNA; 720 BP.

XX AAV61362;  
XX  
DT 18-JAN-1999 (first entry)  
XX Anti-human Fas humanised antibody CH11 VL-RF light chain cDNA.  
XX  
DE Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;  
KW autoimmune disease; rheumatoid arthritis; therapy; human;  
KW antibody engineering; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.

PH Key Location/Qualifiers  
FT sig\_peptide 1..60  
FT /\*tag= a  
FT mat\_peptide 61..717  
FT /\*tag= b

XX EP66131-A2.  
XX  
XX 23-SEP-1998.  
XX  
XX 20-MAR-1998; 98EP-0302113.  
XX  
XX 21-MAR-1997; 97JP-0067938.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;  
XX Yonehara S;  
XX  
XX WPI; 1998-482965/42.  
DR P-PSDB; AAW71879.  
XX

XX Production of anti-Fas protein humanised antibodies - for use in  
PT inducing apoptosis on Fas expressing cells in the treatment of  
PT autoimmune diseases, especially rheumatoid arthritis  
XX  
PS Example 3; Page 100-101; 187pp; English.

XX This cDNA sequence codes for a humanised anti-Fas antibody CH11  
CC light chain (see AAW71879), designated VL-RF. VL-RF is based on the  
CC light chain (see AAW71889) of murine anti-human Fas monoclonal  
XX antibody CH11. The humanised sequence was designed following

CC selection of donor residues from CH11 to be grafted onto acceptor  
CC molecule RPM16410'Cl. 4 Light chain sequences (see AAW71876-79) have  
CC been designed, and each can be used in combination with either of 2  
CC heavy chain sequences (see AAW71880-81) to provide novel, claimed  
CC humanised CH11 IgM antibodies that lack a J chain. These humanised  
CC anti-human Fas antibodies are capable of inducing apoptosis in cells  
CC expressing Fas (e.g. synovialocytes) and are useful in the treatment  
CC of autoimmune disease and chronic rheumatoid arthritis. DNA  
CC sequences encoding the humanised antibodies are claimed, as are  
CC vectors such as pKappaRF2-52 including the VL-RF nucleotide  
CC sequence, and host cells such as Escherichia coli pKappaRF2-52  
XX (FERM BP-5862).

SQ Sequence 720 BP; 177 A; 200 C; 186 G; 157 T; 0 other;

Query Match 86.4%; Score 622; DB 19; Length 720;  
Best Local Similarity 91.6%; Pred. No. 3.8e-156;  
Matches 658; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGTCCAGTGGG 60  
Db 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTAATGCTCTGCGTCCCGGTCCAGTGGG 60  
Qy 61 GAAAGTTGTGATGACTCTCAGTCTCCACTGTCCCTTCCCATCACCTCGAGAGCCGCTCC 120  
Db 61 GATGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACCTCGAGAGCCGCTCC 120  
Qy 121 ATCTCCTGTAGTCTAGTCAAGCTTAAACACAGTAAATGGAGACACCTTCCTGAGTTGG 180  
Db 121 ATCTCCTGCAGTCTAGTAAAGAGCTTGTACACAGTAAATGGAAACACCTATTATCAATTGG 180  
Qy 181 TATCAGCAGAGCCAGGCGCAACCTCCAGGCTCTGATTTATAGGTTTCTTAACCGGGAC 240  
Db 181 TACTTGAGAGAGCCAGGCGCAAGCTCTCAAGGCTCTGATCTACAAAGTTTCCAAACCGATT 240  
Qy 241 TCTGGGTCCCGAGACAGATTTCAGCGCAGTGGGCGAGGACAGATTTTACACTGAAATC 300  
Db 241 TCTGGGTCCCGAGACAGATTTCAGCGCAGTGGGCGAGGACAGTATTCACACTGAAATC 300  
Qy 301 AGCGAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAGACTCCT 360  
Db 301 AGCAGGGTGGAGGCTGAGGATGTTGGGGTTTATTTCTGCTCTCAAAGTACACATGTTCT 360  
Qy 361 CCCACTTTCGGCGGAGGAGCCAAAGTGGAAATCAACGTACGGTGGCTGCACCATCTGTC 420  
Db 361 CCGGGTTTCGGCCAAAGGACCAAGTGGAAATCAACGTACTGTGGCTGCACCATCTGTC 420  
Qy 421 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTCGAACTGCTCTGTTGTGCTG 480  
Db 421 TTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTCGAACTGCTCTGTTGTGCTG 480  
Qy 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATACGCGCTCCAA 540  
Db 481 CTGAATAACTTCTATCCAGAGAGGCGCAAGTACAGTGGAAAGTGGATACGCGCTCCAA 540  
Qy 541 TCGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600  
Db 541 TCGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCCTACAGCCTC 600  
Qy 601 AGCAGCACCTCTGAGCTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660  
Db 601 AGCAGCACCTCTGAGCTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660  
Qy 661 GTCAACCATCAGGCGCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGAGAGTGT 718  
Db 661 GTCAACCATCAGGCGCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGAGAGTGT 718

RESULT 5  
AAA78270  
ID AAA78270 standard; DNA; 720 BP.  
XX  
AC AAA78270;

CC rejection of transplanted organ or tissue for treating proliferative  
CC and hyperproliferative diseases, for treating reversible obstructive  
CC airways disease, intestinal inflammations and allergies e.g. Crohn's  
CC disease and ulcerative colitis, food-related allergies e.g. migraine,  
CC rhinitis and eczema, and other types of allergies. The present nucleic  
CC acid sequence encodes the light chain of 7B6, a primatised antibody  
CC used in the invention to induce apoptosis.

XX  
SQ Sequence 720 BP; 178 A; 200 C; 193 G; 149 T; 0 other;  
Query Match 100.0%; Score 720; DB 24; Length 720;  
Best Local Similarity 100.0%; Pred. No. 2.7e-182; Indels 0; Gaps 0;  
Matches 720; Conservative 0; Mismatches 0;

QY 1 ATGAGGCTCCCTGCTCAGTCTCCGCGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60  
Db |||||  
1 ATGAGGCTCCCTGCTCAGTCTCCGCGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60  
QY 61 GAAGTTGTGATGACTCAGTCTCCATGCTCCCTTCCCATCACCTGGAGCGCGCTCC 120  
Db |||||  
61 GAAGTTGTGATGACTCAGTCTCCATGCTCCCTTCCCATCACCTGGAGCGCGCTCC 120  
QY 121 ATCTCTGTAGTCTAGTCAAGCCCTTAACACAGTAATGGAGACACCTTCTGAGTTGG 180  
Db |||||  
121 ATCTCTGTAGTCTAGTCAAGCCCTTAACACAGTAATGGAGACACCTTCTGAGTTGG 180  
QY 181 TATCAGCAGAGCGAGCCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240  
Db |||||  
181 TATCAGCAGAGCGAGCCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240  
QY 241 TCTGGGGTCCAGACAGATTACGCGCAGTGGGCGAGGACAGATTTCACACTGAAATTC 300  
Db |||||  
241 TCTGGGGTCCAGACAGATTACGCGCAGTGGGCGAGGACAGATTTCACACTGAAATTC 300  
QY 301 AGCGCAGTGGAGGCTGAGATGTTGGGTTTATTCTCGGGCAAGGTACAAGGACTCCT 360  
Db |||||  
301 AGCGCAGTGGAGGCTGAGATGTTGGGTTTATTCTCGGGCAAGGTACAAGGACTCCT 360  
QY 361 CCCACTTTTCGGCGAGGAGCAAGGTTGAAATCAAACTGACGTTGATTAACGCCCTCCAA 420  
Db |||||  
361 CCCACTTTTCGGCGAGGAGCAAGGTTGAAATCAAACTGACGTTGATTAACGCCCTCCAA 420  
QY 421 TTCAATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGCGCTG 480  
Db |||||  
421 TTCAATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGCGCTG 480  
QY 481 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGTGAATACGCCCTCCAA 540  
Db |||||  
481 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGTGAATACGCCCTCCAA 540  
QY 541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600  
Db |||||  
541 TCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600  
QY 601 AGCAGCACTCTGACGCTGAGCAAGAGACTACAGAGAAACAAAGTCTACGCTCGGAA 660  
Db |||||  
601 AGCAGCACTCTGACGCTGAGCAAGAGACTACAGAGAAACAAAGTCTACGCTCGGAA 660  
QY 661 GTCAACCATCAGGCGCTGAGCTCGCGGTACAAAGAGCTTCAACAGGGGAGAGTGTGA 720  
Db |||||  
661 GTCAACCATCAGGCGCTGAGCTCGCGGTACAAAGAGCTTCAACAGGGGAGAGTGTGA 720

RESULT 3  
ID AAT62511 standard; DNA; 720 BP.  
XX AAT62511;  
AC AAT62511;  
XX AC  
XX AC  
DT 25-MAY-1997 (first entry)  
XX AC  
DE Primatised anti-human B7.1 antigen antibody 7B6 light chain DNA.  
XX AC

KW Monoclonal antibody; cynomolgus monkey; macaque; 7B6;  
KW primatised antibody; B7 antigen; CD28; immunosuppressive;  
KW autoimmune disease; idiopathic thrombocytopenia purpura;  
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;  
KW type 1 diabetes mellitus; graft versus host disease;  
KW hetero-hybridoma; transfectoma; ss.  
XX Chimeric Macaca cynomolgus;  
OS Chimeric Homo sapiens.  
XX WO9640878-A1.  
XX 19-DEC-1996.  
XX 06-JUN-1996; 96WO-US10053.  
XX 07-JUN-1995; 95US-0487550.  
XX (IDEC-) IDEC PHARM CORP.  
XX Anderson DR, Brams P, Hanna N, Shestowsky WS;  
XX WPI: 1997-108638/10.  
XX P-PSDB; AAW01819.  
XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -  
XX useful for treating autoimmune disease or graft-versus-host disease  
XX Claim 9; Fig 9A; 81pp; English.

CC 2 DNA sequences (AAT62511 and AAT13847) respectively code for  
CC primatised forms (AAW01819 and AAW01820) of the light and heavy chains  
CC of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody  
CC 7B6. Cloned 7B6 light and heavy variable genes are inserted into  
CC an expression vector (pref. NEOSPLA) which contains human light and  
CC heavy chain constant region genes to allow prodn. of primatised  
CC antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1  
CC antibodies have also been produced (see also AAW01817-18 and AAW01821-  
CC 22). The primatised antibodies inhibit the B7:CD28 pathway, making  
CC them useful immunosuppressants for the treatment of autoimmune  
CC disorders and graft-versus-host disease.  
XX SQ Sequence 720 BP; 178 A; 201 C; 192 G; 149 T; 0 other;

Query Match 99.8%; Score 718.4; DB 18; Length 720;  
Best Local Similarity 99.9%; Pred. No. 7.2e-182;  
Matches 719; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGCCTCCCTGCTCAGTCTCCGCGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60  
Db |||||  
1 ATGAGCCTCCCTGCTCAGTCTCCGCGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60  
QY 61 GAAGTTGTGATGACTCAGTCTCCATGCTCCCTTCCCATCACCTGGAGAGCGCGCTCC 120  
Db |||||  
61 GAAGTTGTGATGACTCAGTCTCCATGCTCCCTTCCCATCACCTGGAGAGCGCGCTCC 120  
QY 121 ATCTCTGTAGGTCTAGTCAAAAGCCTTAAACACAGTAATGGAGACACTTCTGAGTTGG 180  
Db |||||  
121 ATCTCTGTAGGTCTAGTCAAAAGCCTTAAACACAGTAATGGAGACACTTCTGAGTTGG 180  
QY 181 TATCAGCAGAGCCAGGCGACCTCCAGGCTCCTGATTTATAGGTTTCTAACCGGGAC 240  
Db |||||  
181 TATCAGCAGAGCCAGGCGACCTCCAGGCTCCTGATTTATAGGTTTCTAACCGGGAC 240  
QY 241 TCTGGGGTCCAGACAGATTACGCGGCGAGTGGGGCAGGACAGATTTCACACTGAAATTC 300  
Db |||||  
241 TCTGGGGTCCAGACAGATTACGCGGCGAGTGGGGCAGGACAGATTTCACACTGAAATTC 300  
QY 301 AGCGCAGTGGAGGCTGAGATGTTGGGTTTATTCTGCGGGCAAGGTACAAGGACTCCT 360  
Db |||||  
301 AGCGCAGTGGAGGCTGAGATGTTGGGTTTATTCTGCGGGCAAGGTACAAGGACTCCT 360  
QY 361 CCCACTTTTCGGCGAGGAGCAAGGTTGAAATCAAACTGACGTTGATTAACGCCCTCCAA 420

XX Anderson DR, Brams P, Hanna N;  
XX WPI; 1998-286601/25.  
XX P-PSDB; AAW63762.  
XX  
XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and  
XX inhibiting binding to CD28 - useful as specific immunosuppressants  
XX for treating diseases that involve interactions between T and B  
XX cells, e.g. graft rejection or tumours  
XX  
XX Example 7; Fig 4a; 87pp; English.  
XX  
XX This sequence encodes a primatized form of the antibody 7B6 light chain  
XX from macaque. This sequence is used in a method which studies new  
XX monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to  
XX B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such  
XX Mab's are specific immunosuppressants for treatment of diseases involving  
XX T cell/B cell interactions, particularly autoimmune disease, specifically  
XX idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type  
XX I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,  
XX inflammatory bowel disease, allergy and multiple sclerosis, graft vs.  
XX host diseases, B cell lymphoma, infections (including by human immune  
XX deficiency virus) or inflammatory disease and tumours. Optionally the  
XX Mab can be conjugated to a drug or toxin, Mab's, or their fragments, can  
XX also be used as imaging agents and as vaccines or immunogens to develop  
XX anti-idiotypic reagents. Mab's are optionally combined with other proteins  
XX or small molecule immunosuppressants. Blocking B7/CD28 interactions  
XX induces long-term, antigen-specific immunosuppression, i.e. it inhibits  
XX production of interleukin-2 (IL-2), T cell proliferation and  
XX antigen-specific immunoglobulin G (IgG) responses.  
XX  
XX Sequence 720 BP; 178 A; 200 C; 193 G; 149 T; 0 other;

Query Match 100.0%; Score 720; DB 19; Length 720;  
Best Local Similarity 100.0%; Pred. No. 2.7e-182;  
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGCTCCCTGCTCAGCTCTCCGGGCTGCTATTGCTCTGCTCCCGGGTCCAGTGGG 60  
Db 1 ATGAGCTCCCTGCTCAGCTCTCCGGGCTGCTATTGCTCTGCTCCCGGGTCCAGTGGG 60  
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Qy 241 TCTGGGTCCTCAGACAGATTACGCGCAGTGGGGGAGGAGGAGGAGGAGGAGGAGG 300  
Db 241 TCTGGGTCCTCAGACAGATTACGCGCAGTGGGGGAGGAGGAGGAGGAGGAGGAGG 300  
Qy 301 AGCCAGTGGAGGCTGAAGATGTTGGGGTTATTTCTCGGGCAAGGTACAGGACTCCT 360  
Db 301 AGCCAGTGGAGGCTGAAGATGTTGGGGTTATTTCTCGGGCAAGGTACAGGACTCCT 360  
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Db 361 CCCACTTTTCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
Qy 421 TTCACTTTCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
Db 421 TTCACTTTCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
Qy 481 CTGAATTAACCTTATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
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Qy 541 TCGGTTAACTCCAGGAGAGTGTACAGAGCAGGAGCAGCAGCAGCAGCAGCAGCAGCCTC 600  
Db 541 TCGGTTAACTCCAGGAGAGTGTACAGAGCAGGAGCAGCAGCAGCAGCAGCAGCCTC 600  
Qy 601 AGCAGCAGCCTGAGCGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTAGCCTCGGAA 660  
Db 601 AGCAGCAGCCTGAGCGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTAGCCTCGGAA 660  
Qy 661 GTACCCCATCAGGCGCTGAGCTGCCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGTGA 720  
Db 661 GTACCCCATCAGGCGCTGAGCTGCCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGTGA 720

RESULT 2  
AAS17244  
ID AAS17244 standard; DNA; 720 BP.  
AC AAS17244;  
XX 12-MAR-2002 (first entry)  
XX DNA sequence of a primatized form of the light chain of 7B6 antibody.  
XX Human; macaque monkey; light chain; primatized antibody; 7B6 antibody;  
XX neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;  
XX B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;  
XX tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;  
XX graft-vs-host disease; immunosuppression; organ rejection;  
XX interleukin-2; IL-2; mutant; ds.  
XX Chimeric - Homo sapiens.  
OS Chimeric - Macaca sp.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT CDS 1..720  
FT /tags= a  
FT /product= "Light chain of 7B6 antibody"  
XX  
XX W0200189567-A1.  
XX  
XX 29-NOV-2001.  
XX  
XX 22-MAY-2001; 2001WO-US16364.  
XX  
XX 22-MAY-2000; 2000US-0576424.  
XX  
XX (IDEC-) IDEC PHARM CORP.  
XX  
XX Anderson DR, Hanna N, Brams P;  
XX WPI; 2002-089895/12.  
XX P-PSDB; AAU11540.  
XX  
XX Use of monoclonal antibody which specifically binds to B7.1 antigen  
XX CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,  
XX treating cancer, graft-vs-host disease and autoimmune disease such as  
XX allergy -  
XX  
XX Example 8; Fig 4a; 89pp; English.  
XX  
XX The present invention relates to a new use of a monoclonal antibody  
XX which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen  
XX (CD86) for inducing the apoptosis of B7+ cells. The invention is  
XX useful for treating diseases such as B cell cancer, lymphoma, a  
XX cancer where B cells promote the growth and/or metastasis of tumours,  
XX B cell lymphoma, B cell leukaemia, and autoimmune diseases such as  
XX idiopathic thrombocytopenia purpura, systemic lupus erythematosus,  
XX type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic  
XX anaemia, inflammatory bile disease, allergy, multiple sclerosis  
XX or graft-vs-host disease. The antibody is useful for immunosuppression  
XX in a human or animal and for treating or preventing resistance to or

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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 18:12:24 ; Search time 197.594 Seconds  
(without alignments)  
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Title: US-09-758-173-5

Perfect score: 720

Sequence: 1 ATGACCCCTCCCTGCTCAGCT.....TCACAGGGGAGAGTGTGA 720

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	720	100.0	720	19 AAV35486	Macaque primatized
2	720	100.0	720	24 AAS17244	DNA sequence of a
3	718.4	99.8	720	18 AAT62511	Primatized anti-hu
4	622	86.4	720	19 AAV61362	Anti-human Fas hum
5	622	86.4	720	21 AAA78270	Anti-human Fas imm
6	620.4	86.2	891	19 AAV66632	Human immunoglobul
7	620.4	86.2	891	21 AAA78320	Anti-human Fas Ig
8	618.8	85.9	720	19 AAV61360	Anti-human Fas hum
9	618.8	85.9	720	19 AAV61361	Anti-human Fas hum

10	618.8	85.9	720	21 AAA78268	Anti-human Fas imm
11	618.8	85.9	720	21 AAA78269	Anti-human Fas imm
12	617.2	85.7	720	19 AAV61359	Anti-human Fas hum
13	617.2	85.7	720	21 AAA78267	Anti-human Fas imm
14	601.2	83.5	963	22 AAF44895	Human breast cance
15	599.4	83.2	720	21 AAA13924	Human PTHrP monocl
16	599.4	83.2	720	21 AAA13926	Human PTHrP monocl
17	598.8	83.2	720	21 AAA13927	Human PTHrP monocl
18	598.8	83.1	720	21 AAA13923	Human PTHrP monocl
19	596.6	82.9	720	21 AAA13920	Human PTHrP monocl
20	595.4	82.7	720	21 AAA13925	Human PTHrP monocl
21	593.4	82.4	720	21 AAA13922	Human PTHrP monocl
22	591.6	82.2	720	21 AAA13921	Human PTHrP monocl
23	587.8	81.6	720	21 AAA13928	Human PTHrP monocl
24	587.8	81.6	720	21 AAA13929	Human PTHrP monocl
25	582.2	80.9	772	20 AAZ24418	Human bladder tumo
26	561.2	77.9	726	17 AAT18060	Monoclonal antibod
27	558	77.5	720	21 ABK10999	DNA encoding prote
28	554.6	77.0	717	18 AAT62934	Murine anti-porcine
29	554.6	77.0	5300	18 AAT62938	3F4 human IgG4 exp
30	551.6	76.6	925	21 AAA27395	Human IGFAM-15 imm
31	549.2	76.3	740	22 AAF63373	Humanised 323/A3 (
32	549.2	76.3	740	22 AAF63377	Anti-Ep-CAM antibo
33	533	74.0	663	22 AAD20744	Human recombinant
34	527.6	73.3	737	13 AAQ25691	Sequence of the ch
35	520.6	72.3	799	24 AAD32341	Human lung specifi
36	519.2	72.1	727	21 AAZ87965	Chimeric 6G4.2.5 a
37	519.2	72.1	729	16 AAT03380	Anti-IL-8 chimeric
38	519.2	72.1	729	18 AAV03226	Murine variable re
39	519.2	72.1	729	18 AAT93549	Chimeric monoclonal
40	519.2	72.1	729	18 AAT78594	Chimeric monoclonal
41	519.2	72.1	729	19 AAV44951	Anti-IL-8 mouse-hu
42	519.2	72.1	729	19 AAV10316	Chimeric Mab 6G4.2
43	519.2	72.1	729	19 AAV106417	Chimeric monoclonal
44	519.2	72.1	729	20 AAX90573	Chimeric 6G4.2.5 1
45	519.2	72.1	729	21 AAC65504	Murine 6G4-2.5 ant

#### ALIGNMENTS

RESULT 1  
AAV35486  
ID AAV35486 standard; DNA; 720 BP.  
XX  
AC AAV35486;  
XX  
DT 29-SEP-1998 (first entry)  
XX  
DE Macaque primatized 7B6 light chain DNA.

XX Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;  
KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;  
KW T cell/IB cell interaction; tumour; inflammation; imaging agent; vaccine;  
KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;  
KW T cell proliferation; ss.  
XX Macaca fascicularis.

XX  
FH Key Location/Qualifiers  
CDS 1..720  
FT /\*tag= a  
FT /product= 7B6 light chain

XX WO9819706-A1.

XX PD 14-MAY-1998.

XX PF 29-OCT-1997; 97WO-US19906.

XX PR 08-NOV-1996; 96US-0746361.

XX PA (IDEC-) IDEC PHARM CORP.

Qy 718 TGA 720  
Db 733 AGA 735

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Job time : 1373.41 secs

Query Match 78.8%; Score 567.4; DB 12; Length 701;  
 Best Local Similarity 91.5%; Pred. No. 2.1e-154; Indels 1; Gaps 1;  
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QY 61 GAAGTTGTGATGACTCAGCTCTCAGCTCTGCTTCCATCAGCTGGAGAGCGGCTCC 120  
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 92 GATGTTGTGATGACTCAGCTCTCAGCTCTGCTTCCATCAGCTGGAGAGCGGCTCC 151  
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 152 ATCTCTGTAGTCTAGTCTCAAGCCCTTAAACACAGTAATGAGACACCTTCTGAGTTGG 211  
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 Db |||||  
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 Db |||||

QY 361 CCCACTTTTGGGCGGAGGCGCAAGGTGGAATCAACGCTACGCTGGGCTGCACTCTGTC 420  
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 Db |||||

QY 421 TTCAATCTCCCGGCTCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTG 480  
 Db |||||  
 452 TTCAATCTCCCGGCTCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTG 511  
 Db |||||

QY 481 CTGAATTAATCTTATCCAGAGGCGCAAGGTGGAATCAACGCTACGCTGGGCTGCACTCT 540  
 Db |||||  
 512 CTGAATTAATCTTATCCAGAGGCGCAAGGTGGAATCAACGCTACGCTGGGCTGCACTCT 571  
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QY 541 TCGGGTAACTCCAGGAGGAGTGTACAGA-GCAGGACAGGACAGGACAGGACAGGCTTACAGCT 599  
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QY 600 CAGCAGCCTTACGCTGAGCAGGACAGGACAGGACAGGACAGGACAGGACAGGCTTACGCTGCGA 659  
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QY 660 AGTCACCCA 668  
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 VERSION BG740066  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 738)  
 NIH-MGC <http://mgi.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT Robert Strausberg, Ph.D.  
 Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
 Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10628 row: n column: 09  
 High quality sequence stop: 736.  
 Location/Qualifiers  
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 Average insert size 1.5kb. Library constructed by Life  
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Query Match 78.6%; Score 565.8; DB 12; Length 738;  
 Best Local Similarity 90.0%; Pred. No. 6.3e-154; Indels 5; Gaps 4;  
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QY 61 GAAGTTGTGATGACTCAGCTCTCAGCTCTGCTTCCATCAGCTGGAGAGCGGCTCC 120  
 Db |||||  
 75 GATATTGTGATGACCAAGCTCTCTCAGCTGTCACCTTGGACAGCGGCTCC 134  
 Db |||||

QY 121 ATCTCTGTAGTCTAGTCTCAAGCCCTTAAACACAGTAATGAGACACCTTCTGAGTTGG 180  
 Db |||||  
 135 ATCTCTGTAGTCTAGTCTCAAGCCCTTAAACACAGTAATGAGACACCTTCTGAGTTGG 194  
 Db |||||

QY 181 TATCAGCAGAGCCAGGCGCAACCTTCAAGGCTCTGATTTAAGGTTTCTAACCGGGAC 240  
 Db |||||  
 195 CTTCACAGAGCCAGGCGCAGCTCTCAAGCTCTCTCAATTTATAAAATTTCTAACCGGTT 254  
 Db |||||

QY 241 TCTGGGTCCTCAGACAGATTTCAAGGCGAGTGGGCGAGGACAGATTTTCACTGAAATC 300  
 Db |||||  
 255 TCTGGGTCCTCAGACAGATTTCAAGGCGAGTGGGCGAGGACAGATTTTCACTGAAATC 313  
 Db |||||

QY 301 AGGCGAGTGGAGGCTGAGAGATGTTGGGTTTATTTCTGCGGGCAAGGTACAGGACTCT 360  
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 314 AGCAGGTTGGAGCTGAGGATGTTGGGTTTATTTACTGCAATGCAAGTTTCACTTTTCT 373  
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QY 361 CCCACTTTTGGGCGGAGGACCAAGGTGGAATCAAGCTACGCTGGCTGACCACTCTGTC 420  
 Db |||||  
 374 CGAAGCTTGGGCGGAGGACCAAGGTGGAATCAAGCTACGCTGGCTGACCACTCTGTC 432  
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Db	671	AGTCACCACTACAGGCGCTG--AGTCGCGCCCTCAAGAGCTTCAACAGGGAGAGTGT	730
QY	718	T 718	
Db	731	T 731	
RESULT 14			
LOCUS	BG547597	701 bp mRNA linear	EST 04-APR-2001
DEFINITION	602575437F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703696 5',		
ACCESSION	BG547597	mRNA sequence.	
VERSION	BG547597.1	GI:13546262	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1. (bases 1 to 701)		
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LUCM1542 row: i column: 09 High quality sequence stop: 698.		
FEATURES	Location/Qualifiers		
source	1. 701		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:4703696"		
	/clone_lib="NIH_MGC_77"		
	/lab_hosts="DH10B (TI phase-resistant)"		
	/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcgctatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCATTTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."		
BASE COUNT	204 a 266 c 216 g 194 t		
ORIGIN			
	Query Match 79.2%; Score 570.2; DB 12; Length 880;		
	Best Local Similarity 88.8%; Pred. No. 3.7e-155;		
	Matches 640; Conservative 0; Mismatches 78; Indels 3; Gaps 2;		
QY	1	ATGAGCTCCCTGCTCAGCTCTCGGGCTGCTATGCTCTGCGTCCCGGGTCCAGTGGG	60
Db	11	ATGAGGCTCCCTGCTCAGCTCTCGGGCTGCTATGCTCTGCGTCCCGGGTCCAGTGGG	70
QY	61	GAAGTTGTGATGACTCAGTCTCCACGTCCCTTCCCATCACAGCTGGAGCGCGCTCC	120
Db	71	GAAGTTGTGATGACTCAGTCTCCACGTCCCTTCCCATCACAGCTGGAGCGCGCTCC	130
QY	121	ATCTCTGTAGTCTAGTCAAGGCTTAAACACAGTAATGGAGACACCTTCTGAGTTGG	180
Db	131	ATCTCTGTAGTCTAGTCAAGGCTTAAACACAGTAATGGAGACACCTTCTGAGTTGG	190
QY	181	TATCAGCAGAAAGCAGCGCAACTCTCAAGGCTCTGATTTATAAGGTTTCTAAACGGGAC	240
Db	191	TACCTGCAGAAAGCAGCGGCGAGTCTCAACACTCTGATCTATTGGGTTCTAATCGGGCC	250
QY	241	TCGGGGTCCCAACAGATTCACGCGCATGGGGCAGGGACAGATTTACACTGAAATC	300
Db	251	TCGGGGTCCCTGACAGGTTCACTGCGCAGTGGATCAGGCACAGATTTTACACTGAATC	310
QY	301	AGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTCGGGCAAGGTACAGGACTCTCT	360
Db	311	ACAGAAATGGAGGCTGACGATGTTGGGGTTTATTTACTGATGATGATGATGATGATGAT	370
QY	361	CCCACTTTTCGGCGGAGGACCAAGGTGGAAATCAAAACGTTACGCTGCGCATCTGTC	420
Db	371	TTCACTTTTCGGCGGAGGACCAAGGTGGAAATCAAAACGTTACGCTGCGCATCTGTC	430

Db	68	GA	TAT	CGT	GAT	GACT	CA	GCT	CT	CA	CT	CT	CC	T	CC	T	CC	CG	T	CA	CC	CC	T	T	GG	A	G	A	G	C	G	G	C	T	C	C	127
Qy	121	AT	CT	CT	G	T	A	G	G	T	CT	A	A	A	G	C	T	T	A	A	A	C	A	C	A	G	A	C	A	G	A	C	A	C	T	180	
Db	128	AT	CT	CT	G	C	A	G	G	T	CT	A	A	A	G	C	T	T	A	A	A	C	A	C	A	G	A	C	A	G	A	C	A	C	T	187	
Qy	181	TAT	C	A	C	A	G	A	G	C	CA	AGG	CCAA	CT	CC	AA	G	G	CT	C	CT	GA	TTT	TA	A	AG	TTT	TA	A	CC	GG	AC	240				
Db	188	TAC	CT	CA	GA	AG	CC	AGG	CG	AGT	CT	CA	AG	CT	CT	CA	AG	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	247		
Qy	241	T	C	T	G	G	G	T	C	C	A	G	A	G	T	T	C	A	G	G	G	G	G	G	G	G	A	G	A	G	A	G	A	G	A	300	
Db	248	T	C	G	G	G	T	C	C	A	G	T	T	C	A	G	T	T	C	A	G	T	T	C	A	G	T	T	C	A	G	T	T	C	A	307	
Qy	301	A	G	C	A	G	T	G	G	A	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	359		
Db	308	A	G	C	A	G	T	G	G	A	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	367		
Qy	360	T	C	C	A	C	T	T	T	C	G	G	G	A	G	G	A	C	C	A	A	G	T	G	G	A	A	T	C	A	A	A	C	A	C	419	
Db	368	A	T	G	T	A	C	A	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	427		
Qy	420	C	T	T	C	A	T	C	T	T	C	C	G	C	C	A	T	C	T	G	A	T	T	G	A	A	T	C	T	G	A	A	T	C	T	479	
Db	428	C	T	T	C	A	T	C	T	T	C	C	G	C	C	A	T	C	T	G	A	T	T	G	A	A	T	C	T	G	A	A	T	C	T	487	
Qy	480	G	C	T	G	A	T	A	A	C	T	T	A	T	C	C	A	G	A	G	G	C	C	A	A	G	T	A	C	A	G	T	G	A	A	539	
Db	488	G	C	T	G	A	T	A	A	C	T	T	A	T	C	C	A	G	A	G	G	C	C	A	A	G	T	A	C	A	G	T	G	A	A	547	
Qy	540	A	T	C	G	G	T	A	A	C	T	C	C	A	G	A	G	A	G	T	G	T	C	A	G	A	G	A	G	A	G	A	G	A	G	599	
Db	548	A	T	C	G	G	T	A	A	C	T	C	C	A	G	A	G	A	G	T	G	T	C	A	G	A	G	A	G	A	G	A	G	A	G	607	
Qy	600	C	A	G	A	G	A	C	C	T	T	G	A	A	G	C	A	G	A	A	G	C	A	G	A	A	A	C	A	A	A	G	T	C	T	659	
Db	608	C	A	G	A	G	A	C	C	T	T	G	A	A	G	C	A	G	A	A	G	C	A	G	A	A	A	C	A	A	A	G	T	C	T	667	
Qy	660	A	G	T	C	C	A	C	C	A	T	C	A	G	G	C	T	G	A	G	T	C	T	C	C	C	G	T	C	A	A	A	G	A	G	718	
Db	668	A	G	T	C	C	A	C	C	A	T	C	A	G	G																						

RESULT 12	BQ709417	LOCUS	BQ709417	958 bp	mRNA	linear	EST 16-JUL-2002
DEFINITION			AGENCOURT_7976027 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214761 5', mRNA sequence.				

SOURCE	Humani.
ORGANISM	Homo sapiens
REFERENCE	Chordata; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> (bases 1 to 958)
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

high quality sequence: 3/4.	EST 15-MAY-2001
FEATURES	linear
Location/Qualifiers	880 bp mRNA
1..358	602711509F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851723 5', mRNA sequence.
source	DEFINITION
/organism="Homo sapiens"	BG755003
	LOCUS
	BG730003



REFERENCE  
 1 (bases 1 to 908)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM1622 row: b column: 18  
 High quality sequence stop: 725.

# FEATURES

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 /tissue\_type="Primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."  
 BASE COUNT 219 a 250 c 238 g 201 t

Query Match 80.3%; Score 578.4; DB 12; Length 908;  
 Best Local Similarity 90.4%; Pred. No. 1.9e-157;  
 Matches 651; Conservative 0; Mismatches 66; Indels 3; Gaps 3;

QY 1 ATGAGCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGGTCCCGGGTCCAGTGGG 60  
 DB 8 ATGAGGCTCCCTGCTCAGCTCCTCGGGCTGCTAATGCTCTGGGTCTCTGGATCCAGTGGG 67  
 QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCTCCCTCCATCACACCTGGAGAGCGGGCTCC 120  
 DB 68 G-ATATGTGATGACTCAGTCTCCACTCTCCCTGCCGTGACCCCTGGAGAGCGGGCTCC 126  
 QY 121 ATCTCTGTAGGTCTTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCTCTGAGTTGG 180  
 DB 127 ATCTCTGCAGGTCTAGTCAGAGCCTCTGCATAGTAAATGGATACAACTATTGGATTGG 186  
 QY 181 TATCAGCAGAGCCAGGCCAACCCTCAAGCTCTCTGATTTAAGTTTCTAACCGGGAC 240  
 DB 187 TACTCTGAGAAGCCAGG-CAGTCTCCACAGCTCTCTGATCTATTGGGTTCTAATCGGGCC 245  
 QY 241 TCTGGGGTCCACAGACAGATTACCGGCAGTGGGGAGGACAGATTTCACACTGAAATTC 300  
 DB 246 TCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTCACACTGAAATTC 305  
 QY 301 AGCGCAGTGAGGCTGAAGATGTGGGGTTTATTCTCGGGCAAGGTACAAGGACTCTCT 360  
 DB 306 AGCAGAGTGAGGCTGAGGATGTGGGGTTTATTACTGCATGCAAGCTCTACAAATCCG 365  
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 DB 366 CTCACATTTCGGCGGAGGACCAAGTTGGAGATCAAAACGAACTGTGGCTGCACCATCTGTC 425  
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 QY 481 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCCTCCAA 540

DB 486 CTGAATTAACCTCTATCCAGAGAGGCCCAAGATGACAGTGGAGGTGGATAACGCCCTCAA 545  
 QY 541 TCGGGTAACCTCCAGGAGAGTGTTCACAGAGCAGACAGCAAGGACAGCACCTACAGCCTC 600  
 DB 546 TCGGGTAACCTCCAGGAGAGTGTTCACAGAGCAGACAGCAAGGACAGCACCTACAGCCTC 605  
 QY 601 AGCAGCACCTCGAGCTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 660  
 DB 606 AGCAGCACCTCGAGCTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTACGCTCGGAA 665  
 QY 661 GTACCCCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGAGAGTGTGA 720  
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RESULT 11  
 BG758795  
 LOCUS 60271315F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4853557 5',  
 DEFINITION mRNA sequence.

ACCESSION BG758795  
 VERSION BG758795.1 GI:14069448  
 KEYWORDS EST.

SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 859)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM1699 row: m column: 14  
 High quality sequence stop: 724.

# FEATURES

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 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."  
 BASE COUNT 201 a 251 c 215 g 191 t 1 others

Query Match 80.3%; Score 578; DB 12; Length 859;  
 Best Local Similarity 88.6%; Pred. No. 1.9e-157;  
 Matches 637; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

QY 1 ATGAGCTCCCTGCTCAGCTCCTCGGGCTCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60  
 DB 8 ATGAGGCTCCCTGCTCAGCTCCTCGGGCTCTAATGCTCTGGGTCTCTGGATCCAGTGGG 67  
 QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCTCCCTCCATCACACTGGAGAGCGGGCTCC 120

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Db 182 CAGGCCAGTCTCCACAGCTCCCTGATCTATGAAGTTTCCACCGGTTCTCTGGAGTGCCA 241
Qy 253 GACAGATTTCACGCGCAGTGGGAGGAGACAGATTTACACTGAAATACAGCGCAGTGGAG 312
Db 242 GATAGGTTTCACTGGCAGCGGTCAGGACACAGATTTACACTGAAATACAGCGGTTGGAG 301
Qy 313 GCTGAAGATTGGGGTTTATTTCTCGGGGCAAGGTACAAAGACTCTCCACCTTCGGC 372
Db 302 GCTGAGGATGTTGGGGTTTATTACTGTCATGCAAAAGTATACAGCTTCTCTCACTTTCGGC 361
Qy 373 GGAGGACCAAGGTGGAATCAAAAGTACGCTGCTGACCACTCTCTTCACTTTCGGC 432
Db 362 GGAGGGACCAAGGTGGAGTCAAAAGTACGCTGCTGACCACTCTCTTCACTTTCGGC 421
Qy 433 CCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCTGCTGAATTAATTC 492
Db 422 CCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCTGCTGAATTAATTC 481
Qy 493 TATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATTAAGCCCTCAATCGGGTAACTCC 552
Db 482 TATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATTAAGCCCTCAATCGGGTAACTCC 541
Qy 553 CAGAGAGTCTACAGAGCAGGACAGCAAGGACAGCACTTACAGCCTCAGCAGCACCCCTG 612
Db 542 CAGAGAGTCTACAGAGCAGGACAGCAAGGACAGCACTTACAGCCTCAGCAGCACCCCTG 601
Qy 613 ACGTGAGCAAGCAGACTACGAGAAACACAAAGTCTAGCCCTCGAAGTCAACCCATCAG 672
Db 602 ACGTGAGCAAGCAGACTACGAGAAACACAAAGTCTAGCCCTCGAAGTCAACCCATCAG 661
Qy 673 GGCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 718
Db 662 GGCTGAGCTGCGCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 707

RESULT 9
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LOCUS 60305811F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207427 5',
DEFINITION mRNA sequence.
ACCESSION BI768966
VERSION BI768966.1 GI:15760544
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 720)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaops@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11520 row: f column: 04
High quality sequence stop: 719.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5207427"
/clone_lib="NIH_MGC_122"
/lab_host="DH108"
/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
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BASE COUNT 175 a 204 c 185 g 156 t
ORIGIN
Query Match 81.6%; Score 587.2; DB 13; Length 720;
Best Local Similarity 92.1%; Pred. No. 3.5e-160;
Matches 641; Conservative 0; Mismatches 53; Indels 2; Gaps 2;
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Db 26 ATGAGGCTCCCTGCTCAGCTCTCTGGGCTTGTAAATGCTCTGGGTCCAGGATCCAGTGG 85
Qy 60 GGAAGTTGTGATGACTCAGTCTCCACTGTCCTTCCCATCACACTCGAGAGCGGGCTC 119
Db 86 GGATGTTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCACCTTGGACAGCGGGCTC 145
Qy 120 CATCTCTGTAGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCTCTGAGTTG 179
Db 146 CATCTCTGCAGTCTAGTCAAAGCCTCGTATACAGTATGGAAACACCTACTTGAATTG 205
Qy 180 GTATCAGCAGAAGCAGCGCCAACTTCAAGGCTCTGATTTATAGGTTTCTTAACCCGGA 239
Db 206 GTTTTCAGCAGAGGCGAGGCCAATCTCCAAGCGCTTAATTTATAAGGTTTCTTAACCCGGA 265
Qy 240 CTCTGGGGTCCAGACAGATTTCAGCGCAGTGGGGCAGGACAGATTTTCACACTGAAAT 299
Db 266 CTCTGGGGTCCAGACAGATTTCAGCGCAGTGGGTGAGGCTGATTTTCACACTGAAAT 325
Qy 300 CAGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCC 359
Db 326 CAGCAGGGTGGAGGCTGAGGATGTTGGGGTTTATTTACTGCAAGGTACACACTGGCC 385
Qy 360 TCCCACTTTCCGGCGGAGGACCAAGGTGGAAATCAAAGTACGGTGGCTGCACCATCTGT 419
Db 386 GTACACTTTTGGC-CAGGGACCAAGCTGGAGATCAAACGAACCTGTGGCTGCACCATCTGT 444
Qy 420 CTTCACTTTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGGCT 479
Db 445 CTTCACTTTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACCTGCTCTGTTGTGGCT 504
Qy 480 GCTGAATAACTTCTATCCAGAGAGGCCAAAGTAGTACAGTGGAGGTGGATTAACGCCCTCCA 539
Db 505 GCTGAATAACTTCTATCCAGAGAGGCCAAAGTAGTACAGTGGAGGTGGATTAACGCCCTCCA 564
Qy 540 ATCGGGTAACTCCGAGGAGGTGTCACAGCAGGACAGCAGCAGCAGCAGCAGCAGCCT 599
Db 565 ATCGGGTAACTCCGAGGAGGTGTCACAGCAGGACAGCAGCAGCAGCAGCAGCAGCCT 624
Qy 600 CAGCAGCAGCCTGAGCGGTGAGCAAGGACAGACTACGAGAAACACAAAAGTCTACGGCTGGCA 659
Db 625 CAGCAGCAGCCTGAGCGCTGAGCAAGGACAGACTACGAGAAACACAAAAGTCTACGGCTGGCA 684
Qy 660 AGTCAACCCATCAGGCGCTGAGCTCGCCCGTCACAAA 695
Db 685 AGTCAACCCATCAGGCGCTGAGCTCGCCCGTCACAAA 720

RESULT 10
BG685179 908 bp mRNA linear EST 01-MAY-2001
LOCUS 602637065F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764593 5',
DEFINITION mRNA sequence.
ACCESSION BG685179
VERSION BG685179.1 GI:13916576
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2464 row: j column: 02  
High quality sequence stop: 645.  
Location/Qualifiers  
1. .952  
/organism="Homo sapiens"  
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/clone="IMAGE:627729"  
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/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
NIH\_MGC Library."

BASE COUNT 242 a 273 c 252 g 227 t 1 others  
ORIGIN

Query Match 82.2%; Score 591.8; DB 14; Length 995;  
Best Local Similarity 89.3%; Pred. No. 2e-161;  
Matches 634; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1 ATGAGGCTCCCTGCTCAGCTCCAGCTCCAGCTCCCTCCATCACACCTGGAGAGCGCGCTCC 120  
DB 7 ATGAGGCTCCCTGCTCAGCTCCAGCTCCAGCTCCCTCCATCACACCTGGAGAGCGCGCTCC 126  
QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTGTAGTTGG 180  
DB 127 ATCTCTGTAGTCTAGTCAAGCCTTCTGCATAGTAAATGGATCAACATATTTAGATTGG 186  
QY 181 TATCAGCAGAGCCAGGCAACCTCCAAGCTCCTGATTTATAAGTTTCTAACCGGAC 240  
DB 187 TACTCTGAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGC 246  
QY 241 TCTGGGCTCCGACAGATTCAGCGCAGTGGGGCAGGACAGATTTCACTGAAATC 300  
DB 247 TCGGGTCCCTGACAGTTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 306  
QY 301 AGCGAGTGAGGCTGAAGATTTGGGGTTATTTCTCGGGCAAGGTACAAGACTCCT 360  
DB 307 AGCAGATGGAGCTGAGGATTTGGGGTTATTTACTGATGCAAGCTCTACAAATCCG 366  
QY 361 CCCACTTCCGCGGAGGACCAAGTGGAAATCAACAGTACGTTGCTGCTGACCATCTGC 420  
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DB 427 TTTCACTTCCCGGCATCTGATGACGAGTTGAAATCTGGAATCTGCTCTGTGTGTCCTG 486  
QY 481 CTGAATAACTTTCTATCCAGAGAGGCAAGTACAGTGAAGTGGATACGCGCTCCAA 540  
DB 487 CTGAATAACTTTCTATCCAGAGAGGCAAGTACAGTGAAGTGGATACGCGCTCCAA 546  
QY 541 TCGGGTAACTCCAGGAGGTGTCAAGAGCAGGACGAGCAAGGACGACCTACAGCCTC 600  
DB 547 TCGGGTAACTCCAGGAGGTGTCAAGAGCAGGACGAGCAAGGACGACCTACAGCCTC 606  
QY 601 AGCAGCACTCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGAA 660

DB 607 AGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTCGAA 666  
QY 661 GTACCCATCAGGCTGAGCTCGCCGCTCAGAAAGAGCTTCAACAGGG 710  
DB 667 GTACCCATCAGGCTGAGCTCGCCGCTCAGAAAGAGCTTCAACAGGG 716

RESULT 8  
BG758592 952 bp mRNA linear EST 15-MAY-2001  
LOCUS 602712820F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4853045 5',  
DEFINITION mRNA sequence.  
ACCESSION BG758592  
VERSION BG758592.1 GI:14069245  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 952)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM1698 row: h column: 06  
High quality sequence stop: 857.  
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/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
BASE COUNT 233 a 264 c 240 g 215 t  
ORIGIN

Query Match 82.1%; Score 590.8; DB 12; Length 952;  
Best Local Similarity 89.8%; Pred. No. 3.7e-161;  
Matches 634; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 13 GCTCAGTCTCTCGGCTGCTATTTGCTCTGGTCTCCCGGTCAGTGGGAGTTGTGATG 72  
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QY 73 ACTCAGTCTCCAGTCTCCCTCCCATCACACCTGGAGCGGCTCCATCTCCTGTAGG 132  
DB 62 ACCAGACTCCACTCTCTGTCTCGTCCCGTCCAGCGGCTCCATCTCCTCGAAG 121  
QY 133 TCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTCCTGAGTTGGTATCAGAGAAG 192  
DB 122 TCTAGTCAGACCTCTCTGCATAGTGTGGAAGACCTATTATTGTTGTTACCTCGAAG 181  
QY 193 CCAGGCCAAGCTCCAGGCTCCTGATTTATAAGGTTCTTAACCGGGACTCTCGGGTCCCA 252

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Db 241 TGGAGTCCAGATAGGTTCACTGGCAGCGGCTCAGGACAGATTTTCACTGAAATCAG 300
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Qy 363 CACTTTCCGGCGGAGGACCAAGGTGGAAATCAAAAGCTACGGTGGCTGACCAATCTGCTT 422
Db 361 CACTTTCCGGCGGAGGACCAAGGTGGAGATCAAAAGCTGTTGGCTGCACCATCTGCTT 420
Qy 423 CATCTTCCCGGCATCTGTATGAGCAGTTGAAATCTGGAACCTGGAACCTCTGTGTGCTGCT 482
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Qy 663 CACCATCAGGGCTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGG 710
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RESULT 6
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LOCUS 603617168F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440961 5',
DEFINITION mRNA sequence.
ACCESSION BM007723
VERSION 1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs-f@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1914 row: h column: 18
High quality sequence stop: 724.
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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BASE COUNT 181 a 200 c 193 g 152 t
ORIGIN
Query Match 82.3%; Score 592.4; DB 13; Length 726;
Best Local Similarity 90.8%; Pred. No. 1.1e-161;
Matches 654; Conservative 0; Mismatches 61; Indels 5; Gaps 2;
Qy 1 ATGAGCTCCCTCGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG 60
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Qy 61 GAAGTTGATGATCAGTCTCCTGCTCCCTTCCCATCAACCTGGAGAGCGCGCTCC 120
Db 68 GATGTTGATGATCAGTCTCCTGCTCCCTTCCCATCAACCTGGAGAGCGCGCTCC 127
Qy 121 ATCTCTGTAGTGTAGTCAAGCCCTTAAACACAGTAATGAGACACCTTCTCTGAGTTGG 180
Db 128 ATCTCTGTAGTGTAGTCAAGCCCTTAAACACAGTAATGAGACACCTTCTCTGAGTTGG 187
Qy 181 TATCAGCAGAGCCAGGCGCAACCTCCAAGGCTCTCTGATTTATAAGGTTTCTAACCGGAC 240
Db 188 TTTTACAGCAGAGCCAGGCGCAACCTCCAAGGCGCTTAAATTTATAAGGTTTCTAACCGGAC 247
Qy 241 TCTGGGTCCCGACAGATTTACGGGCAAGTGGGGCAGGAGCAGATTTCACTGAAAAATC 300
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Qy 301 AGCGCAGTGGAGGCTGAAGATGTTGGGGTATTATTTCTCGGGGCAAGGTACAAGGACTCCT 360
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Qy 361 CCCACTTTTCGGCGGAGGACCAAG----GTGGAATCAAACTACGTTGCTGCGTGCACCATC 416
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Qy 417 TGTCTTCAATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGTG 476
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Db 608 CCTCAGCAGCAGCTTACGCTGAGCAAGGAGACTACGAGAAACACAAAAGTCTACGCCCTG 667
Qy 657 CGAAGTCAACCATCAGGGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGT 716
Db 668 CGAAGTCAACCATCAGGGCTGAGCTCGCCGTCAGCTCG--CCGTCAAAAAGAGCTTCAACAGGGAGAGTGT 726

RESULT 7
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LOCUS BM012430
DEFINITION AGENCOURT_8352203 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277729
5', mRNA sequence.
ACCESSION BM012430
VERSION BM012430.1 GI:21851329
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
```

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc..  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10611 row: k column: 01  
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/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
Technologies. Note: this is a NCI\_CGAP Library."

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Query Match 82.9%; Score 597.2; DB 12; Length 918;  
Best Local Similarity 91.0%; Pred. No. 4.9e-163;  
Matches 646; Conservative 0; Mismatches 63; Indels 1; Gaps 1;  
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QY 69 GATGACTCAGTCTCCACTGTCCTCCATCCACACTGAGAGAGCGGCTCCATCTCCTG 128  
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DB 121 TAGGTCTAGTCAAGGCTCGTCTATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 180  
QY 189 GAAGCCAGGCAACCTCCAGGCTCTGATTTTATAGGTTTCTAACCGGACTCTGGGCT 248  
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QY 249 CCAGACAGATTGAGGCGAGTGGGCGAGGACAGATTTTCACTGAAATCAGCGCAGT 308  
DB 241 CTCAGACAGATTGAGGCGAGGCGTCAAGCACTGATTTTCACTGAAATCAGCGGCT 300  
QY 309 GGAGGCTGAAGATTTGGGGTTTATTTCTCGGGCAAGGTACAAGACTCTCCCTCCACTTT 368  
DB 301 GGAGGCTGAAGATTTGGGGTTTATTTACTGCATGCAAGGAACACACTGGCCTCACACTTT 360  
QY 369 CGGCGGAGGACCAAGGTGGAATCAAACTAGCTGGGCTGACCACTCTGTCTTATCTT 428  
DB 361 TGCG- CAGGACCAAGTGGAGATCAACGAACTGTGGCTGACCACTCTGTCTTATCTT 419  
QY 429 CCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTGCTGCTGAAATAA 488  
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QY 669 TCAGGGCCTGAGCTCGCCCTCACAAGAGCTTCAACAGGGAGAGCTTT 718  
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DEFINITION 5', mRNA sequence.  
ACCESSION BQ708918  
VERSION BQ708918.1 GI:21847817  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 898)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2518 row: a column: 11  
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/note="Organ: spleen; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
BASE COUNT 202 a 264 c 228 g 203 t 1 others  
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Query Match 82.6%; Score 594.4; DB 14; Length 898;  
Best Local Similarity 90.0%; Pred. No. 3.2e-162;  
Matches 637; Conservative 0; Mismatches 71; Indels 0; Gaps 0;  
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DB 1 GGGGCTCCCTGCTCAGCTCCTCGGCTGCTATTGCTCTGATACCTGGATCCAGTGGGA 60  
QY 63 AGTTGTGATGACTCAGTCTCCACTGTCTCCATCACCCTGGAGAGCCGCGCTCCAT 122  
DB 61 TATTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
QY 123 CTCTGTAGTCTAGTCAAGCCTTAAACAGTAAATGGAGACACCTTCTGAGTGGTA 182  
DB 121 CTCTGCAAGTCTAGTCAGAGCCTTCCATAGTAGTGAAGACCTTTTGTATTGGTA 180  
QY 183 TCAGCAGAGCCAGCCCAACCTCCAGGCTCTGATTTTATAAGGTTTCTAACCGGACTC 242  
DB 181 CTTGAGAGCCAGCCAGCCCTCCAGAGCTCTCTGATGAGTTTCCAAACCGGTTCTC 240  
QY 243 TGGGCTCCAGACAGATTGAGCGCAGTGGGCGAGGACAGATTTTCACTGAAATTCAG 302

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Qy	421	TTCATCTTCGCCGCATCTGATCAGCAGTTGAAATCTGGAATCTGCCCTCTGTTGTGTGCTTG	480
Dd	428	TTCATCTTCGCCGCATCTGATGAGCAGTTGAAATCTGGAATCTGCCCTCTGTTGTGTGCTTG	487
Qy	481	CTGAATAACTTCTATCCCAGAGAGCCAAAAGTACAGTGGAAAGTGGATAACGCCCTCCAA	540
Dd	488	CTGAATAACTTCTATCCCAGAGAGCCAAAAGTACAGTGGAAAGTGGATAACGCCCTCCAA	547
Qy	541	TCGGGTAACTCCCCAGGAGAGTGTACAGAGCAGGACAGCAAAGGACAGCACCTACAGCCTC	600
Dd	548	TCGGGTAACTCCCCAGGAGAGTGTACAGAGCAGGACAGCAAAGGACAGCACCTACAGCCTC	607
Qy	601	AGCAGCACCTTGACGCTGAGCAAAGCAGACTACGAGAAACAACAAAGTCTACGCTGCGAA	660
Dd	608	AGCAGCACCTTGACGCTGAGCAAAGCAGACTACGAGAAACAACAAAGTCTACGCTGCGAA	667
Qy	661	GTCACCATCAGGCGCTGAGCTCGCCCTGACAAAGAGCTTCAACAGGGGAGAGTGT	717
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RESULT 3	
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DEFINITION	mRNA sequence.
ACCESSION	BI758820
VERSION	BI758820.1 GI:15750398
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 857)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: gcapbs-f@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM11457 row: m column: 09 High quality sequence stop: 847.

BASE COUNT  
ORIGIN

BASE C  
ORIGIN

**RESULT 4**  
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 DEFINITION 918 bp mRNA linear EST 01-MAY-2001  
 602627806F1 NCI\_CGAP\_Skn4 Homo sapiens cDNA clone IMAGE:4752888 5',  
 mRNA sequence.  
**ACCESSION**  
 VERSION BG681688  
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 SOURCE EST.  
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 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 918)  
**REFERENCE**  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
**AUTHORS**  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
**TITLE**  
 Unpublished (1999)  
**JOURNAL**



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:54 ; Search time 1370.41 Seconds  
(without alignments)  
8508.978 Million cell updates/sec

Title: US-09-758-173-5  
Perfect score: 720  
Sequence: 1 ATGAGCTCCTCTCAGCT.....TCAACGGGAGAGTGTGA 720

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estnu.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_esti.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_hic.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: gb\_gss.\*

18: em\_gss\_hum.\*

19: em\_gss\_inv.\*

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22: em\_gss\_fun.\*

23: em\_gss\_mam.\*

24: em\_gss\_mus.\*

25: em\_gss\_other.\*

26: em\_gss\_pro.\*

27: em\_gss\_rod.\*

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
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3	598.2	83.1	857	13	BI758820
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					BM007808 603617276
					BI758820 603042739
					BG681688 602627806
					BQ708918 AGENCOURT
					BM007723 603617168

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	591.8	82.2	995	14	BQ712430
8	590.8	82.1	952	12	BG758592
9	587.2	81.6	720	13	BI768966
10	578.4	80.3	908	12	BG685179
11	578	80.3	859	12	BG758795
12	570.6	79.2	958	14	BQ709417
13	570.2	79.2	880	12	BG755003
14	567.4	78.8	701	12	BG547597
15	565.8	78.6	738	12	BG740066
16	564.6	78.4	730	13	BI837183
17	558.6	77.6	753	12	BG756401
18	557.2	77.4	880	12	BG757588
19	555.6	77.2	875	13	BI518518
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21	553.6	76.9	710	13	BI908471
22	549.6	76.3	931	12	BG757255
23	547.4	76.0	696	13	BI838136
24	542.4	75.3	716	13	BI908319
25	542	75.3	912	12	BF974515
26	538.8	74.8	653	10	AW404795
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28	537.4	74.6	962	13	BI819546
29	537	74.6	877	13	BI837569
30	535.8	74.4	934	12	BF974268
31	532	73.9	811	13	BI818338
32	527	73.2	700	12	BG547577
33	512	71.1	709	12	BG757932
34	509.6	70.8	824	13	BI824708
35	505	70.1	990	13	BI838327
36	503	69.9	777	12	BG565315
37	497.8	69.1	735	12	BF238157
38	497.4	69.1	904	14	BQ711273
39	496.8	69.0	964	12	BG757678
40	492.6	68.4	689	14	BM768355
41	490.8	68.2	1075	12	BG758924
42	490.4	68.1	634	14	BM783161
43	490.4	68.1	923	14	BQ711051
44	489.4	68.0	683	12	BG745349
45	489.4	68.0	881	14	BQ709375

## ALIGNMENTS

RESULT 1  
BI759427  
LOCUS BI759427 816 bp mRNA linear EST 25-SEP-2001  
DEFINITION G03043095F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5183446 5', mRNA sequence.  
ACCESSION BI759427  
VERSION BI759427.1 GI:15751005  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 816)  
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-x@mail.nih.gov](mailto:cgabs-x@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: L1AM11457 row: n column: 23  
High quality sequence start: 2  
High quality sequence stop: 814.  
Location/Qualifiers

BI759427 816 bp mRNA linear EST 25-SEP-2001  
G03043095F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5183446 5',  
mRNA sequence.  
BI759427  
BI759427.1 GI:15751005  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 816)  
<http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-x@mail.nih.gov](mailto:cgabs-x@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: L1AM11457 row: n column: 23  
High quality sequence start: 2  
High quality sequence stop: 814.  
Location/Qualifiers



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DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR KIM: KIM00001; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 32.5%; Score 403.5; DB 1; Length 131;
Best Local Similarity 59.8%; Pred. No. 4.5e-26;
Matches 79; Conservative 20; Mismatches 32; Indels 1; Gaps 1;

Qy 1 MSLPAQLLGLLLLCVPGSGEVWMTQSPISLTPEPAPISCSRSSQSLKHSNGDTPLSW 60
Db 1 METDTLLWLLWVPGSTGNIVLTQSPASLAVSLGQRATISCRASESV-DSYGNFMHW 59

Qy 61 YQKPGQPPRLLIYKVSNRDSCVDPDFSGAGTDFTLKISAVEAEDVGVECGQGRTP 120
Db 60 YQKPGQPPKLLIYLAASMLESGVPARTFSGSGRTDFTLTIDPVEADDAATYCCQNNEDP 119

Qy 121 PTFGGTKVEIK 132
Db 120 WTFGGTKLEIK 131

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Search completed: March 29, 2003, 09:11:14  
Job time : 6.69846 secs

RA Marsh P., Mills F., Gould H.;  
 RT "Detection of a unique human V kappa IV germline gene by a cloned  
 RL cDNA probe.";  
 RN Nucleic Acids Res. 13:6531-6544 (1985).  
 RP REVISION TO 76.  
 RA Marsh P.;  
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBSJ databases.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X02990; CAA26733.1; -;  
 DR PIR; A01905; K4HUL7.  
 DR HSP; P80362; 1WTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.  
 FT DOMAIN 21 43 FRAMEWORK-1.  
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 61 75 FRAMEWORK-2.  
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 83 114 FRAMEWORK-3.  
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 122 133 FRAMEWORK-4.  
 FT DISULFID 43 114 BY SIMILARITY.  
 FT NON TER 134 134  
 SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;  
 Query Match 33.1%; Score 411.5; DB 1; Length 134;  
 Best Local Similarity 61.4%; Pred. No. 1.1e-26;  
 Matches 82; Conservative 23; Mismatches 26; Indels 1; Gaps 1;  
 QY 1 MSLPAQLGLLLCVPGSGEVVNTQSLPITPGEPASISCRSSQSLKHSNGD-TFLS 59  
 Db 1 MYLQTVFISLLWISGAGDIWNTQSPDLSVSLGERATINCKSGSILYSSONKNYLA 60  
 QY 60 WYQKPGOPPLLIYKVNRSNDSGVDPFSGSGAGTDTFLKISAVEADVGVYFCQGTRT 119  
 Db 61 WYQKPGOPPLLIYWASTRESGVDPFSGSGAGTDTFLKISAVEADVGVYFCQYYNL 120  
 QY 120 PTFGGTKVEIKR 133  
 Db 121 PWTFGGKVEIKR 134  
 RESULT 14  
 ID KV2E MOUSE STANDARD; PRT; 113 AA.  
 AC P03976;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region 17S29.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN REVISIONS.  
 RP MEDLINE=79012520; PubMed=6441768;  
 RA McKean D.J., Ball M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 RL related mouse kappa variable regions.";  
 DR Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).  
 DR PIR; A01935; KVM5M6.  
 DR HSP; P01679; 2FBU.  
 DR InterPro; IPR003006; Ig\_MHC.

RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the  
 RT group A-streptococcal polysaccharide";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383 (1984).  
 CC -1. MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.  
 DR PIR; A01912; KVM517.  
 DR HSP; P01607; 1REI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 40 54 FRAMEWORK-2.  
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 62 93 FRAMEWORK-3.  
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 103 112 FRAMEWORK-4.  
 FT DISULFID 23 93 BY SIMILARITY.  
 FT NON TER 113 113  
 SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;  
 Query Match 32.5%; Score 404; DB 1; Length 113;  
 Best Local Similarity 68.1%; Pred. No. 3.4e-26;  
 Matches 77; Conservative 14; Mismatches 22; Indels 0; Gaps 0;  
 QY 21 EVMTQSPFLSLPITPGEPASISCRSSQSLKHSNGD-TFLSWYQKPGOPPLLIYKVNRS 80  
 Db 1 DIVMTQAVFNPVTLGTSASISCRSSQSLKHSNGITYLYWYQKPGOSQQLLYQMSNLA 60  
 QY 81 SGVDPFSGSGAGTDTFLKISAVEADVGVYFCQGTRTPTFGGKVEIKR 133  
 Db 61 SGVDPFSGSGAGTDTFLKISAVEADVGVYCAHNLELPTVFGGKLEIKR 113  
 RESULT 15  
 ID KV3I MOUSE STANDARD; PRT; 131 AA.  
 AC P01661;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region MOPC 63 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN REVISIONS.  
 RP MEDLINE=78235887; PubMed=98179;  
 RA Burstein Y., Schechter I.;  
 RT "Primary structures of N-terminal extra peptide segments linked to  
 RT the variable and constant regions of immunoglobulin light chain  
 RT precursors: implications on the organization and controlled  
 RT expression of immunoglobulin genes.";  
 RL Biochemistry 17:2392-2400 (1978).  
 RN [2]  
 RP SEQUENCE OF 21-131.  
 RA MEDLINE=73140225; PubMed=4691517;  
 RA McKean D.J., Potter M., Hood L.E.;  
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among  
 RT kappa chains with limited sequence differences.";  
 RL Biochemistry 12:760-771 (1973).  
 RN [3]  
 RP REVISIONS.  
 RP MEDLINE=79012520; PubMed=99744;  
 RA McKean D.J., Ball M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 RL related mouse kappa variable regions.";  
 DR Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).  
 DR PIR; A01935; KVM5M6.  
 DR HSP; P01679; 2FBU.  
 DR InterPro; IPR003006; Ig\_MHC.



DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.  
 FT DOMAIN 21 43 FRAMEWORK-1.  
 FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 44 55 FRAMEWORK-2.  
 FT DOMAIN 56 70 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 71 77 FRAMEWORK-3.  
 FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 110 118 JKI SEGMENT.  
 FT DOMAIN 119 129 BY SIMILARITY.  
 FT DISULFID 43 109  
 FT NON TER 129 129  
 SQ SEQUENCE 129 AA; 14073 MW; D3C552927772774D0 CRC64;  
 Query Match 34.0%; Score 422; DB 1; Length 129;  
 Best Local Similarity 62.4%; Pred. No. 1.4e-27;  
 Matches 83; Conservative 21; Mismatches 25; Indels 4; Gaps 1;  
 QY 1 MSLPAQLGLLLCVPGSSGEVVMVTPGEPASISCRSSQSLKHSNGDFTFLW 60  
 DB 1 METPAQLFLLLMLPDTGTGIVLTQSGTSLSPGERATLSRASQSVSS----YLAW 56  
 QY 61 YQOKPGQPRLIIYKVSNRDGVDPFRSGSGAGTDFTLKISAVEAEDGVYFCGQGTTP 120  
 DB 57 YQOKPGQAPRLIIYKVSNRDGVDPFRSGSGAGTDFTLKISAVEAEDGVYFCGQGTTP 116  
 QY 121 PTFGGGTKEIKR 133  
 DB 117 RTFGGGTKEIKR 129  
 RESULT 9  
 KV2A HUMAN  
 ID KV2A HUMAN STANDARD; PRT; 115 AA.  
 AC P01614;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-II region Cum.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=68242259; PubMed=5586923;  
 RA Hilschmann N.;  
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
 RN [2]  
 RP REVISIONS TO 50; 52; 96 AND 97.  
 RX MEDLINE=70063440; PubMed=4188189;  
 RA Hilschmann N.;  
 RT "Molecular basis of antibody formation.";  
 RL Naturwissenschaften 56:195-205(1969).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01885; K2HUCM.  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR003006; IGV\_MHC.  
 DR InterPro; IPR003596; IGV\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DISULFID 24 95  
 FT NON TER 115 115  
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;  
 Query Match 33.9%; Score 420.5; DB 1; Length 115;  
 Best Local Similarity 71.9%; Pred. No. 1.6e-27;  
 Matches 82; Conservative 15; Mismatches 16; Indels 1; Gaps 1;

QY 21 EVVMTQSPPLSLPITPGEPASISCRSSQSLKHS-NGDTFLSWYQKPGQPPRLIIYKVSNR 79  
 DB 2 DIVMTQSPPLSLPITPGEPASISCRSSQSLSDGNTYLNWYLOKAGSPOLLITLSYR 61  
 QY 80 DSGVPRFRFGSGAGTDFTLKISAVEAEDGVYFCGQGTTPPTFGGGTKEIKR 133  
 DB 62 ASGVPRFRFGSGSGTDFTLKISRVQAEADVGVYVCWQRLIEIPVTFGGGTKEIRR 115  
 RESULT 10  
 KV4B HUMAN  
 ID KV4B HUMAN STANDARD; PRT; 133 AA.  
 AC P06313;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-IV region JI precursor.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041853; PubMed=2997712;  
 RA Klobeck H.G.; Bornkamm G.W.; Combriato R.; Pohlenz H.D.;  
 RA Zachau H.G.;  
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a single germline gene.";  
 RL Nucleic Acids Res. 13:6515-6529(1985).  
 CC -----  
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 CC -----  
 DR EMBL; Z00022; CAA77317.1; -.  
 DR PIR; A01904; K4HUIJ.  
 DR HSSP; P80362; IWTU.  
 DR InterPro; IPR003006; IGV\_MHC.  
 DR InterPro; IPR003596; IGV\_V.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.  
 FT DOMAIN 21 43 FRAMEWORK-1.  
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 61 75 FRAMEWORK-2.  
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 83 114 FRAMEWORK-3.  
 FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 123 132 FRAMEWORK-4.  
 FT DISULFID 43 114 BY SIMILARITY.  
 FT NON TER 133 133  
 SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;  
 Query Match 33.8%; Score 420; DB 1; Length 133;  
 Best Local Similarity 64.2%; Pred. No. 2.1e-27;  
 Matches 86; Conservative 19; Mismatches 27; Indels 2; Gaps 2;  
 QY 1 MSLPAQLGLLLCVPGSSGEVVMVTPGEPASISCRSSQSLKHSNGDFTFLW 59  
 DB 1 MVLQTVFTSLLSWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLA 60  
 QY 60 YQOKPGQPRLIIYKVSNRDGVDPFRSGSGAGTDFTLKISAVEAEDGVYFCGQGTTP 119  
 DB 61 YQOKPGQPRLIIYKVSNRDGVDPFRSGSGAGTDFTLKISAVEAEDGVYFCGQGTTP 119  
 QY 120 PTFGGGTKEIKR 133

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SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;
Query Match 36.5%; Score 453; DB 1; Length 113;
Best Local Similarity 75.2%; Pred. No. 3.7e-30;
Matches 85; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLIYKVSNRD 80
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Db 1 DIVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLIYKVSNR 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 81 SGVPDRFSGSGAGTDFTLKISAVEADVGVYFCQGTRTPPTFGGKTKVEIKR 133
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Db 61 SGVPDRFSGSGGTDFTLKISRVEADVGVYCMZALQAPITFGGKTRLEIKR 113
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RESULT 6
KV2B_HUMAN
ID KV2C_HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
some facts and a unifying hypothesis."
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01887; K2HUMD.
DR HSSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 102 111 FRAMEWORK-4.
FT NON TER 112 112 BY SIMILARITY.
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 34.9%; Score 433.5; DB 1; Length 112;
Best Local Similarity 69.9%; Pred. No. 1.4e-28;
Matches 79; Conservative 18; Mismatches 15; Indels 1; Gaps 1;

QY 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLIYKVSNRD 80
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Db 1 DIVLTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLIYKVSNR 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 81 SGVPDRFSGSGAGTDFTLKISAVEADVGVYFCQGTRTPPTFGGKTKVEIKR 133
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Db 60 SGVPDRFSGSGGTDFTLKISRVAZBVGYYCMQALQPLTLFGGKTNVEIKR 112
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RESULT 7
KV2B_HUMAN
ID KV2B_HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
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DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Riessen W.F., Jaton J.-C.;
MEDLINE=76253627; PubMed=821524;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine."
RL Biochemistry 15:3829-3833(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUPR.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 123 93 BY SIMILARITY.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 34.6%; Score 430; DB 1; Length 113;
Best Local Similarity 71.7%; Pred. No. 2.7e-28;
Matches 81; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLIYKVSNRD 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVVMTQSPFLPVLTPGEPASIQCRSSQSLVYRBCGTYLVBWLKPGQSPPELLIYLSVYRD 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 81 SGVPDRFSGSGAGTDFTLKISAVEADVGVYFCQGTRTPPTFGGKTKVEIKR 133
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPDRFSDSGGTDFTLKTRVQAEADVGVYCMQATZSPYTFGGTKLZIKR 113
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kipps T.J., Tomhave E., Chen P.E., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy."
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
DR PIR; P10022; K3HUHA.
DR HSSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1;
```



QY 61 YQKPGQPPRLIIKYNSRDSVDPFSGSGAGTDTFTLKISAVEADGVYFCQGTRTP 120  
 Db 61 FQKPGQSPRLIIKYNSRDSVDPFSGSGAGTDTFTLKISAVEADGVYFCQGTHWS 120  
 QY 121 PTFGGGKTKVEIKR 133  
 Db 121 WTFGGGKTKVEIKR 133

RESULT 2  
 KAC\_HUMAN STANDARD; PRT; 106 AA.  
 AC P01834;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig kappa chain C region.  
 GN IGKC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE (MYELOMA PROTEIN EU).  
 RX MEDLINE=71064023; PubMed=5489770;  
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino  
 acid sequence of the light chain."  
 RL Biochemistry 9:3155-3161(1970).  
 RN [2]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 Intra-chain disulfide bonds."  
 RL Biochemistry 9:3188-3196(1970).  
 RN [3]  
 RP SEQUENCE (BENCE-JONES PROTEIN TI).  
 RX MEDLINE=72188439; PubMed=5027703;  
 RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein  
 TI). IV. The complete amino acid sequence and its significance for  
 the mechanism of antibody production."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81042304; PubMed=6775818;  
 RA Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;  
 RT "Cloned human and mouse kappa immunoglobulin constant and J region  
 genes conserve homology in functional segments."  
 RL Cell 22:197-207(1980).  
 RN [5]  
 RP SEQUENCE (BENCE-JONES PROTEIN ROY).  
 RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,  
 Steinmetz-Kayne M., Suter L., Watanabe S.;  
 RL (In) Franek F., Shugar D. (eds.);  
 RL Gamma Globulins: structure and function, pp.57-74, Academic Press,  
 RL New York (1969).  
 RN [6]  
 RP SEQUENCE (BENCE-JONES PROTEIN CUM).  
 RX MEDLINE=68242259; PubMed=5586923;  
 RA Hilschmann N.;  
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-  
 type)."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
 RN [7]  
 RP SEQUENCE (BENCE-JONES PROTEIN AG).  
 RX MEDLINE=69234734; PubMed=4893682;  
 RA Titani K., Shinoda T., Putnam F.W.;  
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The  
 complete sequence and the location of the disulfide bridges."

J. Biol. Chem. 244:3550-3560(1969).  
 RN [8]  
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).  
 RX MEDLINE=70201507; PubMed=5447531;  
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;  
 RT "Macroglobulin structure: variable sequence of light and heavy  
 chains".  
 RL Science 169:56-59(1970).  
 CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,  
 CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC  
 CC MARKER, 45-ALA AND 83-LEU.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; J00241; AAA58989.1; -;  
 DR EMBL; V00557; CAA23823.1; -;  
 DR PIR; A02116; K3HU.  
 DR HSP; P01842; 7FAB.  
 DR Genew; HGNC:5716; IGKC.  
 DR MIM; 147200; -;  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00407; IGc1; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 1  
 FT DISULFID 26 86  
 FT DISULFID 106 106  
 FT VARIANT 83 83  
 FT INTERCHAIN (WITH A HEAVY CHAIN).  
 FT V -> L (IN INV(1,2) MARKER).  
 FT /FTID=VAR\_003897.  
 FT CONFLICT 14 14 D -> N (IN REF. 7 AND 8).  
 FT CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).  
 SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;  
 Query Match 44.1%; Score 548; DB 1; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-38;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 134 TVAAPSVFIFPSPDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 193  
 Db 1 TVAAPSVFIFPSPDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
 QY 194 KOSTYSLSLTSLTKADYKHKYKACVTHQGLSSPVTKSPNRGEC 239  
 Db 61 KOSTYSLSLTSLTKADYKHKYKACVTHQGLSSPVTKSPNRGEC 106  
 RESULT 3  
 KV2E HUMAN STANDARD; PRT; 117 AA.  
 ID KV2E HUMAN  
 AC P06309;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region GM607 precursor (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84191506; PubMed=6325927;  
 RA Klobeck H.G., Solomon A., Zachau H.G.;  
 RT "Contribution of human V kappa II germ-line genes to light-chain  
 RT diversity."  
 RL Nature 309:73-76(1984).







Best Local Similarity 61.4%; Pred. No. 2.1e-42;  
Matches 135; Conservative 34; Mismatches 50; Indels 1; Gaps 1;

Qy 21 EYVMTQSPSLPITPGEPAISCRSSQSLKHSNGD-TFLSWYQQKPGOPPRLLIYKVN 79  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|  
Db 1 DIVMTQSPSSLVTAGEKVTWMSCTSSQSLFNSGKQNYLTWYQQKPGOPPKVLIYWA 60  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|

Qy 80 DSGVDRFSGSGAGDTFTLKISAVBAEDVGVYFCGGGTTPPTFGGKTKEIKRTVAAPS 139  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|  
Db 61 ESVGDRFRTSGSGDFTLTISVQAEDLAVVYCYQNDYSNPLTFGGGKTLEKLRADAAPT 120  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|

Qy 140 VFIPPSDEQLSGTASVVCLLNNFPYPREAKVQWKVDNALGSGNSQESVTEODSKDSTYS 199  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|  
Db 121 VSIFFPSSEQLTSGGASVVCFLNNFPYKIDINVKKIDGSRQNGVLNSWTQDQSKDSTYS 180  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|

Qy 200 LSSLTLSKADYKEHKVYACEVTHOGLSPVTKSFNRGEC 239  
:|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|  
Db 191 MSSLTLTKDEYERNHSYTCEATHKTSPIVKSFNREK 220  
:|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|

RESULT 14  
S37484  
Ig kappa chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 11-Jan-2000  
C:Accession: S37484  
R:Ducancel, F.P.D.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S37483  
A:Accession: S37484  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-225 <DUC>  
A:Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 56.5%; Score 702; DB 2; Length 225;  
Best Local Similarity 58.5%; Pred. No. 6.1e-41;  
Matches 134; Conservative 37; Mismatches 52; Indels 6; Gaps 2;

Qy 11 LLLCPGSSGEVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFTLSWYQQKPGOPPR 70  
|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|  
Db 3 LLLCVSAGHSIVMTQTPTKFLLSAGDRVTITCKASQSVSND----VAMYQQKPGQSPK 57  
|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|

Qy 71 LLIVKVNDRDGVDRFSGSGAGDTFTLKISAVBAEDVGVYFCGGGTTPPTFGGKTKE 130  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|  
Db 58 LLIVYASRYTGVPDRFRTSGSGDFTFTISTVQAEDLAVVYFC-QDYSSYTFGGGKTLE 116  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|

Qy 131 IKRTVAAPSVFIPPPSDEQLSGTASVVCLLNNFPYPREAKVQWKVDNALGSGNSQESVTE 190  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|  
Db 117 IKRDAAPTIVFIPPSSEQLTSGGASVVCFLNNFPYKIDINVKKIDGSRQNGVLNSWTD 176  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|

Qy 191 QDSKDSYVLSSTLTLSKADYKEHKVYACEVTHOGLSPVTKSFNRGEC 239  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|  
Db 177 QDSKDSYVMSSTLTLTKDEYERNHSYTCEATHKTSPIVKSFNREK 225  
:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|

RESULT 15  
S68241  
Ig kappa chain V region (Mab13-1) - mouse (fragment)  
N:Alternate names: immunoglobulin light chain  
C:Species: Mus musculus (house mouse)  
C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C:Accession: S68241; S68214  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Im  
submitted to the EMBL Data Library, March 1994  
A:Description: Specific peroxidase activity by formation of an antibody L-chain  
A:Reference number: S68241  
A:Accession: S68241  
A:Molecule type: mRNA  
A:Residues: 1-218 <TAK>  
A:Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963

```
RESULT 10
S42772
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53236.1; PID:g414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 64.0%; Score 795; DB 2; Length 217;
Best Local Similarity 68.7%; Pred. No. 2.8e-47;
Matches 149; Conservative 26; Mismatches 42; Indels 0; Gaps 0;

QY 23 VNTQSLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIYKVNRSRG 82
Db 1 VNTQSLSLPVLGDAQASISCRSSQSLVHTNGNTYLHWYLPKQPGQPKVLIYKVSTRESG 60

QY 83 VPRFSGSGAGTDFTLKISAVEAEDVGVYFCGGQTRTPPTFGGKTKVEIKRTVAAPS 142
Db 61 VPRFSGSGGTDFTFKLSRVEAEDLGVYFCQSQTIVPFTFGSGTKLEIKRADAAPTVSI 120

QY 143 PPSDEQLKGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDYSLSS 202
Db 121 PPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQGVNLNSWTQDQSKDYSSNS 180

QY 203 TLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 181 TLTLYKDEYERHNSYTCETHTKTSTSPVKSFNREGC 217

RESULT 11
JL0029
Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a anti-phospho
A:Reference number: JL0029; MUID:88171315; PMID:3127529
A:Accession: JL0029
A:Molecule type: mRNA
A:Residues: 1-225 <CHI>
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A:Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because
ect except for four positions shown above
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:7-225/Product: Ig kappa chain #status predicted <ILC>
F:7-106/Domain: V region #status predicted <VAR>
F:107-119/Domain: J region #status predicted <ILR>
F:120-225/Domain: C region #status predicted <COR>

Query Match 62.0%; Score 770; DB 2; Length 225;
Best Local Similarity 64.7%; Pred. No. 1.5e-45;
Matches 143; Conservative 32; Mismatches 46; Indels 0; Gaps 0;

QY 19 SGEVMTQSLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIYKVN 78
Db 5 SSDVLTQIPLSLPVLGDAQASISCRSSQSLVHTNGNTYLHWYLPKQPGQPKVLIYK 64
```

```
QY 79 RDSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGGQTRTPPTFGGKTKVEIKRTVAAP 138
Db 65 RFGVDPDRFSGSGGTDFTLSLEISRVEAEDLGVYCYQSSHVRTWTFGGTKLEIKRADAAP 124

QY 139 SVFTFPSPDQLKGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDYSLSS 198
Db 125 TVSIPTPSTLQSGGASVVCFLNNFYPKDINVKKIDGSRQGVNLNSWTQDQSKDYSLSS 184

QY 199 SLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 185 SMSSTLTLYKDEYERHNSYTCETHTKTSTSPVKSFNREGC 225

RESULT 12
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 61.6%; Score 765.5; DB 2; Length 240;
Best Local Similarity 61.7%; Pred. No. 3.1e-45;
Matches 148; Conservative 34; Mismatches 57; Indels 1; Gaps 1;

QY 1 MSLPAQLGLLLCVPGSSGEVMTQSLSLPITPGEPASISCRSSQSLKHS-NGDTFLS 59
Db 1 MESQTQVLMSLLLWISGTCGDFVMTQSPSLAVSAGETVTINCKSSQSLFYSGNKVLA 60

QY 60 WYQKFGQPPRLIYKVNRSRGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGGQTRT 119
Db 61 WYQKFGQPKLLIYWASTRQSGVDPDRFSGSGGTDFTLTSSVQAEALAIYCLQYVET 120

QY 120 PTFGGGKTKVEIKRTVAAPSVIFPPSPDEQLKGTASVCLNNFYPRKAVQKVDNAL 179
Db 121 PTFGGAGTKLEIKRADAAPTIVSIFPSTEQATGATGASVVCVCLNNFYPRDISVKWKIDGTE 180

QY 180 QSGNSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 181 RRDGVLDSTVDQDSKDYSSMSSTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 13
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an ant
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:W23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 58.3%; Score 723.5; DB 2; Length 220;
```

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-219 <VAN>  
A:Cross-references: EMBL:L35138; NID:G522336; PIDN:AAA67525.1; PID:G522337  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 66.0%; Score 820; DB 2; Length 219;  
Best Local Similarity 69.4%; Pred. No. 5.6e-49;  
Matches 152; Conservative 28; Mismatches 39; Indels 0; Gaps 0;  
  
QY 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80  
DB 1 DVVMTQSPSLPVSIGDQASISCRSSQSLVHSNGNTLYWYLRKPGQSPKLLIYVSNRF 60  
  
QY 81 SGVPRFSGSGAGDTFTLKISAVEAEDGVVYFCGGQTRTPPTFGGQTKVEIKRTVAAPSV 140  
DB 61 SGVPRFSGSGAGDTFTLKISAVEAEDGVVYFCGGQTRTPPTFGGQTKVEIKRTVAAPSV 120  
  
QY 141 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTYL 200  
DB 121 SIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTYL 180  
  
QY 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SSTLTLTDEYERHNSYTCATHKTSPIVKSFNNEC 219

## RESULT 7

PC4203  
Ig kappa chain (monoclonal antibody MAbA34) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 11-Jan-2000  
C:Accession: PC4203  
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.  
Gene 173, 257-259, 1996  
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody MAbA34  
A:Reference number: PC4203; MUID:97082978; PMID:8964510  
A:Accession: PC4203  
A:Molecule type: mRNA  
A:Residues: 1-219 <KWA>  
A:Cross-references: GB:U29147; NID:G1594225; PIDN:AAC52821.1; PID:G1594226  
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density lipoprotein (HDL).  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:1-112/Domain: V region #status predicted <VRG>  
F:113-219/Domain: C region #status predicted <CRG>

Query Match 65.0%; Score 807; DB 2; Length 219;  
Best Local Similarity 68.0%; Pred. No. 4.3e-48;  
Matches 149; Conservative 31; Mismatches 39; Indels 0; Gaps 0;  
  
QY 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80  
DB 1 DVVMTQSPSLPVSIGDQASISCRSSQSLVHSNGNTLYWYLRKPGQSPKLLIYVSNRF 60  
  
QY 81 SGVPRFSGSGAGDTFTLKISAVEAEDGVVYFCGGQTRTPPTFGGQTKVEIKRTVAAPSV 140  
DB 61 SGVPRFSGSGAGDTFTLKISAVEAEDGVVYFCGGQTRTPPTFGGQTKVEIKRTVAAPSV 120  
  
QY 141 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTYL 200  
DB 121 SIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTYL 180  
  
QY 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SSTLTLTDEYERHNSYTCATHKTSPIVKSFNNEC 219

## RESULT 8

S16112  
Ig kappa chain V region (G2a) - mouse  
C:Species: Mus musculus (house mouse)

C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S16112  
R:Vaesen, M.; Prosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.; F. Biol. Chem. Hoppe-Seyler 372, 451-453, 1991  
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(2-macroglobulin)  
A:Reference number: S16112; MUID:92000313; PMID:1910583  
A:Accession: S16112  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-219 <BIT>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 806; DB 2; Length 219;  
Best Local Similarity 68.9%; Pred. No. 5e-48;  
Matches 151; Conservative 28; Mismatches 40; Indels 0; Gaps 0;  
  
QY 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80  
DB 1 DVVMTQSPSLPVSIGDQASISCRSSQSLVHSNGNTLYWYLRKPGQSPKLLIYVSNRF 60  
  
QY 81 SGVPRFSGSGAGDTFTLKISAVEAEDGVVYFCGGQTRTPPTFGGQTKVEIKRTVAAPSV 140  
DB 61 SGVPRFSGSGAGDTFTLKISAVEAEDGVVYFCGGQTRTPPTFGGQTKVEIKRTVAAPSV 120  
  
QY 141 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTYL 200  
DB 121 SIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTYL 180  
  
QY 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SSTLTLTDEYERHNSYTCATHKTSPIVKSFNNEC 219

## RESULT 9

S38865  
Ig kappa chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 15-Jun-2001  
C:Accession: S38865  
R:Kipp, B.; Becker, W.; Schlaak, M.  
submitted to the EMBL Data Library, November 1993  
A:Description: Combination of a defined specificity and desired isotype by cloning of an antibody gene.  
A:Reference number: S38864  
A:Accession: S38865  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-219 <KIP>  
A:Cross-references: EMBL:Z27396; NID:G416538; PIDN:CAAB1787.1; PID:G416539  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 64.1%; Score 796; DB 2; Length 219;  
Best Local Similarity 68.9%; Pred. No. 2.4e-47;  
Matches 151; Conservative 26; Mismatches 42; Indels 0; Gaps 0;  
  
QY 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80  
DB 1 ELVMTQSPSLPVSIGDQASISCRSSQSLVHSNGNTLYWYLRKPGQSPKLLIYVSNRF 60  
  
QY 81 SGVPRFSGSGAGDTFTLKISAVEAEDGVVYFCGGQTRTPPTFGGQTKVEIKRTVAAPSV 140  
DB 61 SGVPRFSGSGAGDTFTLKISAVEAEDGVVYFCGGQTRTPPTFGGQTKVEIKRTVAAPSV 120  
  
QY 141 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTYL 200  
DB 121 SIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTYL 180  
  
QY 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SSTLTLTDEYERHNSYTCATHKTSPIVKSFNNEC 219

Query Match 73.1%; Score 908; DB 2; Length 215;  
 Best Local Similarity 79.9%; Pred. No. 5.7e-55;  
 Matches 175; Conservative 19; Mismatches 21; Indels 4; Gaps 1;

Qy 21 EVVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKQPGQPPRLLIYKVNRD 80  
 Db 1 EIVLTQSPGTLSPGERATLSRASQSVN---YLAWYQKQPGQAPSLIYDASSRA 56  
 Qy 81 SGVPDRFSGSGAGTDFTLKISAVEAEADVGVFCGQGRTPPTFGGKTKVEIKRTVAAPSV 140  
 Db 57 TGIPIRFGSGSGGTDFTLTISRLEPEDFAVYVYQYQYSGSPFTFGGKTKVEIKRTVAAPSV 116  
 Qy 141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYL 200  
 Db 117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYL 176  
 Qy 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
 Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 3  
 JE0243  
 Ig kappa chain NIG93 precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
 C:Accession: JE0243  
 R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, H.; T  
 submitted to JIPID, November 1998  
 A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy  
 A:Reference number: JE0243  
 A:Accession: JE0243  
 A:Molecule type: protein  
 A:Residues: 1-215 <ALI>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 876; DB 2; Length 215;  
 Best Local Similarity 77.7%; Pred. No. 8.5e-53;  
 Matches 171; Conservative 18; Mismatches 25; Indels 6; Gaps 2;

Qy 21 EVVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKQPGQPPRLLIYKVNRD 80  
 Db 1 EIVMTQSPATLSVSPGERATLSRASQSVN---TNVVMYQKQPGQAPRLIYDASTRA 55  
 Qy 81 SGVPDRFSGSGAGTDFTLKISAVEAEADVGVFCGQGRTPPTFGGKTKVEIK-RTVAAPS 139  
 Db 56 TGVPAERFSGSGGTEFTLTISRLEQSEDAFYVYVYQYQHNNAPPTFGQGTVEIKRTVAAPS 115  
 Qy 140 VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYL 199  
 Db 116 VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYL 175  
 Qy 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
 Db 176 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 4  
 A23746  
 Ig kappa chain V-III (KAU cold agglutinin) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
 C:Accession: A23746  
 R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.  
 J. Biol. Chem. 266, 2836-2842, 1991  
 A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl  
 A:Reference number: A23746; MUID:91131575; PMID:1993660  
 A:Accession: A23746  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-215 <LEO>

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 860; DB 2; Length 215;  
 Best Local Similarity 78.4%; Pred. No. 1e-51;  
 Matches 171; Conservative 18; Mismatches 25; Indels 4; Gaps 1;

Qy 21 EVVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKQPGQPPRLLIYKVNRD 80  
 Db 1 EIVLTQSPATLSVSPGERATLSRASQSVN---SSNYLAWYQKQPGQAPRLIYDASSRA 56  
 Qy 81 SGVPDRFSGSGAGTDFTLKISAVEAEADVGVFCGQGRTPPTFGGKTKVEIKRTVAAPSV 140  
 Db 57 TGIPIRFGSGSGGTDFTLTISRLEPEDFAVYVYQYQYSGSPFTFGGKTKVEIKRTVAAPSV 116  
 Qy 141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYL 200  
 Db 117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYL 176  
 Qy 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
 Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 5  
 JE0241  
 Ig kappa chain Am37 precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
 C:Accession: JE0241  
 R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
 submitted to JIPID, November 1998  
 A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mult  
 A:Reference number: JE0241  
 A:Accession: JE0241  
 A:Molecule type: protein  
 A:Residues: 1-216 <ALI>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 841.5; DB 2; Length 216;  
 Best Local Similarity 76.7%; Pred. No. 1.9e-50;  
 Matches 168; Conservative 21; Mismatches 27; Indels 3; Gaps 3;

Qy 21 EVVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKQPGQPPRLLIYKVNRD 80  
 Db 1 DIVLTQSPDPLAVSLGERATINCKSSQSVLY-NSKNFLAWYQKQPGQ-PKLLIW-ANVRE 57  
 Qy 81 SGVPDRFSGSGAGTDFTLKISAVEAEADVGVFCGQGRTPPTFGGKTKVEIKRTVAAPSV 140  
 Db 58 SGVPDRFSGSGGTDFTLTISRLEQSEDAFYVYVYQYQHNNAPPTFGQGTVEIKRTVAAPSV 117  
 Qy 141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYL 200  
 Db 118 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYL 177  
 Qy 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
 Db 178 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 6  
 S52028  
 Ig kappa chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
 C:Accession: S52028  
 R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirks, W.G.; Schots, A.; I  
 submitted to the EMBL Data Library, August 1994  
 A:Description: Coordinates expression of antibody subunit genes yields high levels of func  
 A:Reference number: S52028  
 A:Accession: S52028

GenCore version 5.1.4 p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 10.7265 Seconds  
(without alignments)  
2141.995 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSLLPAQLGLLLLCVPGSSG.....EVTHQGLSSPVTKSFNRGEC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	915	73.7	215	2 JE0244	Ig kappa chain NIG
2	908	73.1	215	2 JE0242	Ig kappa chain NIG
3	876	70.5	215	2 JE0243	Ig kappa chain NIG
4	860	69.2	215	2 A23746	Ig kappa chain V-I
5	841.5	67.8	216	2 JE0241	Ig kappa chain Am3
6	820	66.0	219	2 S2028	Ig kappa chain - m
7	807	65.0	219	2 PC4203	Ig kappa chain (no
8	806	64.9	219	2 S16112	Ig kappa chain v r
9	796	64.1	219	2 S38865	Ig kappa chain - m
10	795	64.0	217	2 S42772	Ig kappa chain - m
11	770	62.0	225	2 JL0029	Ig kappa chain pre
12	765.5	61.6	240	2 S06084	Ig kappa chain pre
13	723.5	58.3	220	2 A31290	Ig kappa chain v r
14	702	56.5	225	2 S37484	Ig kappa chain - m
15	694.5	55.9	218	2 S68241	Ig kappa chain v r
16	688.5	55.4	214	2 S68212	Ig kappa chain (Ma
17	688.5	55.4	218	2 JC5810	monoclonal antibod
18	687.5	55.4	234	2 S14237	Ig kappa chain pre
19	686	55.2	197	2 S29593	Ig kappa chain (WM
20	684.5	55.1	234	2 S01320	Ig kappa chain pre
21	680	54.8	230	2 S33161	Ig kappa chain - s
22	662.5	53.3	210	2 S25058	Ig kappa chain v r
23	644	51.9	235	2 S25058	Ig kappa chain - m
24	617	49.7	178	2 PT0219	Ig kappa chain V-C
25	599	48.2	135	2 S20559	JC-kappa protein -
26	572	46.1	229	2 A20969	Ig kappa chain pre
27	565.5	45.5	140	2 S22658	Ig kappa chain pre
28	552	44.4	133	2 S22320	Ig kappa chain pre
29	552	44.4	133	2 S42611	HUNVK protein prec

## ALIGNMENTS

### RESULT 1

JE0244

Ig Kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 915; DB 2; Length 215;

Best Local Similarity 80.9%; Pred.No.1.9e-55;

Matches 178; Conservative 19; Mismatches 17; Indels 6; Gaps 3;

Qy 21 EVVMTQSPLSLPTFGEPASISCRSSQSLKHSNGDTFLSWYQQKFGQPPRLIYKVSNRD 80

Db 1 EVVLTQSPATLSVSPGERATLSCRASQSV-HSN---LAWYQQKPGQAPRLIYRASTRA 55

Qy 81 SGVDPDFSSGAGDTFTLKISAVEADVGIVFCGCGTTPP-TFGSGTKVETKRTVAAPS 139

Db 56 TGIPARFSSGSGDTFTLTSLQSEDFALYYCQYNTWPPITFGGTVKIKRTVAAPS 115

Qy 140 VFIPTPSDQLKSGTASVVCLLNNFYPREAKQVQKVDNALQSGNSQESVTEQDSKDSYSTS 199

Db 116 VFIPTPSDQLKSGTASVVCLLNNFYPREAKQVQKVDNALQSGNSQESVTEQDSKDSYSTS 175

Qy 200 LSSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 239

Db 176 LSSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 215

### RESULT 2

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mult

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-91/Domain: immunoglobulin homology <IMM>

Search completed: April 6, 2003, 06:25:19  
Job time : 37.7832 secs



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QY 238 GACTCTGGGGTCCAGACAGAGATTTCAGCGCAGTGGGCGAGGACAGATTTCACACTGAAA 297
Db 1254 GAATCTGGGGTACCTGACCGAATTCAGTGGCAGCGGCTCGGACAGAGATTTCACCTCACC 1313
QY 298 ATCAGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAAGACT 357
Db 1314 ATCAGCAGCTGCAGGCTGAAGATGTGGCAGTATACACTGTCAAGATGTTCTAGATTTT 1373
QY 358 CTCCACTTTTCGGCGGAGGACCAAGGTGGAATCAAAAGTACGGTGGTGCACCACTCT 417
Db 1374 CCATTCACGTTTCGGCGGAGGACCAAGTTGGAGATCAAAAGTACGTTGTCGGCGGCCATCT 1433
QY 418 GTCTTCATCTTCCCGCCATCTGATGACAGTGTGAATCTGGAATCTGGAATCTGTTGTGTC 477
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QY 538 CAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGACAGCAAGGACACCTACAGC 597
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QY 598 CTCAGCAGCAGCTGAGCGCTGAGCAAGAGCAGCTACAGAGAAAACAAAGTCTACGCCCTGC 657
Db 1614 CTCAGCAGCAGCTGAGCGCTGAGCAAGAGCAGCTACAGAGAAAACAAAGTCTACGCCCTGC 1673
QY 658 GAAGTACCCCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 717
Db 1674 GAAGTACCCCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 1733
QY 718 TGA 720
Db 1734 TAA 1736
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RESULT 15  
US-08-940-371-50  
; Sequence 50, Application US/08940371  
; Patent No. 5851525  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P. O. Box 1539-UW2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/940,371  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/470,110  
; FILING DATE:

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; APPLICATION NUMBER: US 08/363131  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50282  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270-5024  
; TELEFAX: 610 270-5090  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5703 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
US-08-940-371-50  
  
Query Match 68.0%; Score 489.4; DB 2; Length 5703;  
Best Local Similarity 80.8%; Pred. No. 6.4e-135;  
Matches 584; Conservative 0; Mismatches 136; Indels 3; Gaps 1;  
  
QY 1 ATGAGCCTCCCTGCTCAGCTCTCGGGCTGCTATTTGCTCTCGGTCCCGGGTCCAGTGGG 60  
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QY 61 GAAAGTGTGATGACTCAGCTCTCCACTGCTCCCTTCCCATCACACCTGGAGAGCCGCGCTCC 120  
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Db 1134 ATCAACTGCAAGAGCTCTCAGAGTCTGTAAACAGTGGAAATCAAAAGAACTACTTGGCC 1193  
QY 178 TGGTATCAGCAGAGCCAGGCAACCTCCAGGCTCTCTGATTTATTAAGTTTCTTAACCGG 237  
Db 1194 TGGTATCAGCAGAGAACCCGCGGCGCTCTTAAGTTGTCTATTACGGGGCGTCACTAGG 1253  
QY 238 GACTCTGGGGTCCCAGACAGATTTCAGCGGCGAGTGGGGCAGGACAGAGATTTTCACACTGAAA 297  
Db 1254 GAATCTGGGGTACCTGACCGATTTCAGTGGCAGCGGCTCGGACAGAGATTTCACTCTCACC 1313  
QY 298 ATCAGCGCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGCGGGCAAGGTACAAAGACT 357  
Db 1314 ATCAGCAGCTGCAGGCTGAAGATGTGGCAGTATACACTGTCAAGATGTTCTAGATTTT 1373  
QY 358 CCTCCACTTTTCGGCGGAGGACCAAGGTGGAATCAAAAGTACGGTGGTGCACCACTCT 417  
Db 1374 CAATTCAGTTCGGCGGAGGACCAAGTTGGAGATCAAAAGTACTGTGAGATCAAAAGTACT 1433  
QY 418 GTCTTCATCTTCCCGCCATCTGATGACAGTGTGAATCTGGAATCTGTTGTGTC 477  
Db 1434 GTCTTCATCTTCCCGCCATCTGATGACAGTGTGAATCTGGAATCTGTTGTGTC 1493  
QY 478 CTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAGTGGAGTGGATTAACGCCCTC 537  
Db 1494 CTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAGTGGAGTGGATTAACGCCCTC 1553  
QY 538 CAATCGGGTAACTCCAGGAGAGTGTCAAGAGCAGACAGCAAGGACAGCACTACAGC 597  
Db 1554 CAATCGGGTAACTCCAGGAGAGTGTCAAGAGCAGACAGCAAGGACAGCACTACAGC 1613  
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Db 1614 CTCAGCAGCAGCTGAGCGCTGAGCAAGAGCAGCTACAGAGAAAACAAAGTCTACGCCCTC 1673  
QY 658 GAAGTACCCCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 717  
Db 1674 GAAGTACCCCATCAGGCGCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT 1733  
QY 718 TGA 720  
Db 1734 TAA 1736
```



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; INFORMATION FOR SEQ ID NO: 50:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 5703 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: circular
;
; MOLECULE TYPE: DNA (genomic)
US-08-470-110A-50

```

Query Match	68.0%	Score 489.4	DB 1	Length 5703
Best Local Similarity	80.8%	Pred. No. 6.4e-135		
Matches 584	Conservative	0	Mismatches 136	Indels 3
QY	1	ATCAGCCTCCCTGCTCAGCTCTCGGGTGTATTGCTCTCGTCCCGGGTCCAGTGGG	60	
DB	1014	ATGGTGTGAGACCAGGCTTTCATTTCTCTGTGTCTGGATCTCTGTGCTCTACGGG	1073	
QY	61	GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACTGAGAGCGGGCTCC	120	
DB	1074	GATATCGTGATGACCCAGTCTCCAGACTCGTAGTGTGTCTCTGGSCGAGAGGGCCACC	1133	
QY	121	ATCTCTGTAGGTCTAGTCAAAAGCCTTAAACACAGT---AATGAGACACCTTCCTGAGT	177	
DB	1134	ATCAACTGCAAGAGCTCTCAGAGTCTGTAAACAGTGGAAATCAAAAGAACTACTTTGGCC	1193	
QY	178	TGCTATTACAGACAGGACGAGCCAACTCCAAAGGTCCTGATTATTAAGTTTCTTAACCGG	237	
DB	1194	TGCTATCAGCAGNAAACCGGGCAGCTCTAAGTTGCTCATTTACGGGGCGTCCGACTAGG	1253	
QY	238	GACTCTGGGGTCCCAGACAGATTACAGCGCAGTGGGCGAGGACAGATTTCAACACTGAAA	297	
DB	1254	GAATCTGGGGTACTTGACCGATTAGTGGCAGCGGCTGGGACAGATTTCACTCTCACCC	1313	
QY	298	ATCAGCGCAGTGGAGCTGAAGATCTTGGGCTTTATTTCTCGGGCAGGTAACAGGACT	357	
DB	1314	ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTATACTACTGTCCAGAAATGTTCAATGTTT	1373	
QY	358	CTTCCCACTTTTCGGCGGAGGGACCAAGGTGGAAATCAAACTACGGTGGCTGCACCATCT	417	
DB	1374	CCATTACGTTTCGGCGGAGGGACCAAGTTGGAGATCAACCGTACTGTGGCGGGCCATCT	1433	
QY	418	GTCTTCATCTTCCGGCATCTGATGAGCAGTTTGAATCTGGAACCTGCTCTGTGTGTGC	477	
DB	1434	GTCTTCATCTTCCGGCATCTGATGAGCAGTTTGAATCTGGAACCTGCTCTGTGTGTGC	1493	
QY	478	CTGCTCAATAACTTTCTATCCAGAGAGGCCAAAGTACAGTGGGAAGTGGATAACGCCCTC	537	
DB	1494	CTGCTGAATAACTTTATCCAGAGAGGCCAAAGTACAGTGGGAAGTGGATAACGCCCTC	1553	
QY	538	CAATCGGGTAACCTCCAGGAGAGTGTCTACAGAGCAGGACAGCAAGGACACCTACAGC	597	
DB	1554	CAATCGGGTAACCTCCAGGAGAGTGTCTACAGAGCAGGACAGCAAGGACACCTACAGC	1613	
QY	598	CTCAGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAAACAAGTCTACGGCTGC	657	
DB	1614	CTCAGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAAACAAGTCTACGGCTGC	1673	
QY	658	GAAGTCAACCCATCAGGGCTTGAGCTCGGCCGTCAAAAGAGCTTTCAACAGGGAGAGTGT	717	
DB	1674	GAAGTCAACCCATCAGGGCTTGAGCTCGGCCGTCAAAAGAGCTTTCAACAGGGAGAGTGT	1733	
QY	718	TGA	720	
DB	1734	TAA	1736	

RESULT 14  
US-08-667-769A-50  
; Sequence 50, Application US/08667769A  
; Patent No. 5783184  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.

1 APPLICANT: Chaiken, Irwin M.  
 2 APPLICANT: Cook, Richard M.  
 3 APPLICANT: Gross, Mitchell S.  
 4 APPLICANT: Holmes, Stephen D.  
 5 APPLICANT: McMillan, Lynette J.  
 6 APPLICANT: Theisen, Timothy W.  
 7  
 8 TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
 9 TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
 10  
 11 NUMBER OF SEQUENCES: 76  
 12  
 13 CORRESPONDENCE ADDRESS:  
 14 ADDRESSEE: SmithKline Beecham Corp./Corporate  
 15 STREET: P.O. Box 1539-UW2220  
 16 CITY: King of Prussia  
 17 STATE: Pennsylvania  
 18 COUNTRY: USA  
 19  
 20 ZIP: 19406-0939  
 21  
 22 COMPUTER READABLE FORM:  
 23 MEDIUM TYPE: Floppy disk  
 24 COMPUTER: IBM PC compatible  
 25 OPERATING SYSTEM: PC-DOS/MS-DOS  
 26  
 27 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 28  
 29 CURRENT APPLICATION DATA:  
 30 APPLICATION NUMBER: US/08/667,769A  
 31 FILING DATE:  
 32 CLASSIFICATION: 424  
 33  
 34 PRIOR APPLICATION DATA:  
 35 APPLICATION NUMBER: PCT/US95/17082  
 36 FILING DATE: 22-DEC-1995  
 37  
 38 PRIOR APPLICATION DATA:  
 39 APPLICATION NUMBER: US 08/470110  
 40 FILING DATE: 06-JUN-1995  
 41  
 42 PRIOR APPLICATION DATA:  
 43 APPLICATION NUMBER: US 08/467420  
 44 FILING DATE: 06-JUN-1995  
 45  
 46 PRIOR APPLICATION DATA:  
 47 APPLICATION NUMBER: US 08/363131  
 48 FILING DATE: 23-DEC-1994  
 49 ATTORNEY/AGENT INFORMATION:  
 50 NAME: Sutton, Jeffrey A.  
 51 REGISTRATION NUMBER: 34,028  
 52 REFERENCE/DOCKET NUMBER: P50503  
 53 TELECOMMUNICATION INFORMATION:  
 54 TELEPHONE: 610-270-5024  
 55 TELEFAX: 610-270-5090  
 56  
 57 INFORMATION FOR SEQ ID NO: 50:  
 58 SEQUENCE CHARACTERISTICS:  
 59 LENGTH: 5703 base pairs  
 60 TYPE: nucleic acid  
 61 STRANDEDNESS: double  
 62 TOPOLOGY: circular  
 63  
 64 MOLECULE TYPE: DNA (genomic)  
 65 US-08-667-769A-50

Query Match	68.0%;	Score 489.4;	DB 1;	Length 5703;
Best Local Similarity	80.8%;	Pred. No. 6.4e-135;		
Matches 584; Conservative	0;	Mismatches 136;	Indels 3;	Gaps 1;

Qy	1	ATGAGCCTCCCTGCTCAGTCTCTCGGGTGCTATTGCTCTCGGTCCCGGGTCCAGTGGG	60
Db	1014	ATGGTGTTCAGACCCAGGCTCTTCAATTTCTCTGTTGCTCTGGATCTCTGTGGCTACGGG	1073
Qy	61	GAAGTTGTGATGACTCAGTCTCCACTGTGTCCTTCCATCACACTGGAGAGCGGCGCTCC	120
Db	1074	GATATGTTGATGACCCAGTCTCCAGACTGCTAGTGCTGTCTTCGGGGGAGGGGCCACC	1133
Qy	121	ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGT---AATGGAGACACCTTCTCCTGAGT	177
Db	1134	ATCAACTGCAAGACTCTCAGAGTCTGTTTAAACAGTGGAAATCAAAAGAACTACTTGGCC	1193
Qy	178	TGTTATCAGCAGAGCCAGCGCCAACTCCAGGCTCTGATTTATAGGTTTCTTAACCGG	237
Db	1194	TGTTATCAGCAGAAACCGGGCAGCGCTCTTAAGTTGCTCATTTACGGGGCGCTCGACTAGG	1253

APPLICANT: Appelbaum, Edward R.  
APPLICANT: Chaiken, Irwin M.  
APPLICANT: Cook, Richard M.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Holmes, Stephen D.  
APPLICANT: McMillan, Lynette J.  
APPLICANT: Theisen, Timothy W.  
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
TREATMENT OF IL5 Mediated Disorders  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
STREET: P. O. Box 1539-UM2220  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,420A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/363131  
FILING DATE: 23-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50282  
TELEPHONE: 610 270-5024  
TELEFAX: 610 270-5090  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5703 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-467-420A-50

Query Match 68.0%; Score 489,4; DB 1; Length 5703;  
Best Local Similarity 80.8%; Pred. No. 6,4e-135;  
Matches 584; Conservative 0; Mismatches 136; Indels 3; Gaps 1;  
QY 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGGCTCCCGGGTCCAGTGGG 60  
DB 1014 ATGGTGTTCAGACCCAGGCTTCATTCTCTGCTCTGGATCTCTGGTGCCTACGGG 1073  
QY 61 GAAGTTGTGATGACTGATCTCAGCTCCTCCCTCCATCACCTCGAGAGCGGGCTCC 120  
DB 1074 GATATCGTGATGACCCAGTCTCCAGACTCGCTAGCTGTGCTCTGGCGGAGAGGGCCACC 1133  
QY 121 ATCTCCGTGAGTCTAGCTAAAGCTTTAAACACAGT---AATGGACACCTTCCTGAGT 177  
DB 1134 ATCACTGCAAGAGCTCTAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTTGGCC 1193  
QY 178 TGGTATCAGCAGAGGAGCGGACCACTCCAGGCTCCTGATTTTAAAGTTTCTAACCGG 237  
DB 1194 TGGTATCAGCAGAAACCCGGGAGCTCCTAAGTTGCTATTTACGGGGCTCGACTAGG 1253  
QY 238 GACTCTGGGTCCAGACAGATTTCAGCGGAGTGGGCGAGGACAGATTTCACTGAA 297  
DB 1254 GAATCTGGGTACCTGACCGATTTCAGTGGAGCGGGTCTGGGACAGATTTCACTCTCACC 1313  
QY 298 ATCAGCGCAGTGGAGGCTGAAGATGTTGGGTTTATTTCTGCGGGCAAGGTACAAAGACT 357  
DB 1314 ATCAGCAGCTGCAGGCTGAAGATGTCGAGTATATCTACTGTCTAGATGTTTCATAGTTT 1373

QY 358 CTCTCCACTTTTCGGCGGAGGACCAAGGTGGAATCAAAAGTACGGTGGCTGCACCATCT 417  
DB 1374 CCAATTCAGTTTCGGCGGAGGACCAAGTTGGAGATCAAAAGTACTGTGGCGGGCCATCT 1433  
QY 418 GTCTTTCATCTTCGGCCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTGTGTGC 477  
DB 1434 GTCTTTCATCTTCGGCCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTGTGTGC 1493  
QY 478 CTGCTGAATAACTTTCTATCCAGAGAGCCAAAGTACAGTGGAGGTGGATAACGCCCTC 537  
DB 1494 CTGCTGAATAACTTTCTATCCAGAGAGCCAAAGTACAGTGGAGGTGGATAACGCCCTC 1553  
QY 538 CAATCGGGTAACTCCAGAGAGTGTTCAGAGAGGACAGCAGGACAGCAGCTACAGC 597  
DB 1554 CAATCGGGTAACTCCAGAGAGTGTTCAGAGAGGACAGCAGGACAGCAGCTACAGC 1613  
QY 598 CTCAGCAGCAGCCCTGAGCTGAGCAAAAGCAGACTTACGAGAAACACAAAGTCTACGCCCTGC 657  
DB 1614 CTCAGCAGCAGCCCTGAGCTGAGCAAAAGCAGACTTACGAGAAACACAAAGTCTACGCCCTGC 1673  
QY 658 GAAGTCAACCATCAGGCGCTGAGCTCGCCCTGCACAAAGAGCTTCAACAGGGGAGAGTGT 717  
DB 1674 GAAGTCAACCATCAGGCGCTGAGCTCGCCCTGCACAAAGAGCTTCAACAGGGGAGAGTGT 1733  
QY 718 TGA 720  
DB 1734 TAA 1736

## RESULT 13

US-08-470-110A-50  
Sequence 50, Application US/08470110A  
Patent No. 5693323  
GENERAL INFORMATION:  
APPLICANT: Ames, Robert S.  
APPLICANT: Appelbaum, Edward R.  
APPLICANT: Chaiken, Irwin M.  
APPLICANT: Cook, Richard M.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Holmes, Stephen D.  
APPLICANT: McMillan, Lynette J.  
APPLICANT: Theisen, Timothy W.  
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
TREATMENT OF IL5 Mediated Disorders  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P. O. Box 1539-UM2220  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,110A  
FILING DATE:  
CLASSIFICATION: 426  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/363131  
FILING DATE: 23-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50282  
TELEPHONE: 610 270-5024  
TELEFAX: 610 270-5090



APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/026,985  
FILING DATE: 20-Feb-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085R3-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 729 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
US-09-026-985-41

Query Match 72.1%; Score 519.2; DB 3; Length 729;  
Best Local Similarity 86.7%; Pred. No. 4.4e-144;  
Matches 572; Conservative 0; Mismatches 86; Indels 0; Gaps 0;  
QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTCCATCACACCTGGAGAGCGGCTCC 120  
DB 70 GATATCGTATGACACAGACCACTCTCCCTGCTGTCAGTCTTGGAGATCAGGCTCC 129  
QY 121 ATCTCTGTAGTCTAGTCAAGCTTAAACAGTAATGGAGACACCTTCTGAGTTGG 180  
DB 130 ATCTCTGTAGTCTAGTCAAGCTTAAACAGTAATGGAGACACCTTCTGAGTTGG 189  
QY 181 TATCAGCAGAGCCAGGCGCAACCTCCAAAGCTCTCTGATTTATAAGTTTCTAAACGGGAC 240  
DB 190 TACCTGCAGAGCCAGGCGCAACCTCTCCAAAGCTCTCTGATTTCTAAACGGGATTT 249  
QY 241 TCTGGGCTCCAGACAGATTTCAGGCGCAGTGGGAGGACAGATTTCACACTGAAATC 300  
DB 250 TCTGGGCTCCAGACAGATTTCAGGCGCAGTGGGAGGACAGATTTCACACTGAGGATC 309  
QY 301 AGCAGCTGAGGCTGAGATGTTGGGGTTTATTTCTGGGGCAAGGTACAGGACTCTCT 360  
DB 310 AGCAGCTGAGGCTGAGATGTTGGGGTTTATTTCTGGGGCAAGGTACAGATGTTCCG 369  
QY 361 CCACATTTCCGCGGAGGACAGAGTGGAAATCAACAGTACCGTGGCTGCACATCTGTC 420  
DB 370 CTCACGTTCCGCTGCTGGGACCAAGCTGGAGCTGAAACGGGCTGTTGCTGCACCAACTGA 429  
QY 421 TTCACTCTCCGCGCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGSCCTG 480  
DB 430 TTCACTCTCCGCGCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGSCCTG 489  
QY 481 CTGAATAACTTCTATCCAGAGGCGCAAGTACAGTGAAGTGGATACCGCTCTCAA 540  
DB 490 CTGAATAACTTCTATCCAGAGGCGCAAGTACAGTGAAGTGGATACCGCTCTCAA 549  
QY 541 TCGGGAATCTCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACTTACAGCTTC 600

DB 550 TCGGTAACTCCAGAGAGTGTCTACAGAGAGGACACAAAGGACAGCACTTACAGCTC 609  
QY 601 AGCAGCACCTCTGACCTGAGCAAGCAGACTACGAGAAACACAAAGTCTAGCCTTGGCAA 660  
DB 610 AGCAGCACCTCTGACCTGAGCAAGCAGACTACGAGAAACACAAAGTCTAGCCTTGGCAA 669  
QY 661 GTACCCATCAGGCTGAGCTGCGCCCTTCAAAAGAGCTTCAACAGGGAGAGTTGA 720  
DB 670 GTACCCATCAGGCTGAGCTGCGCCCTTCAAAAGAGCTTCAACAGGGAGAGTTGA 729  
RESULT 10  
US-09-121-952A-41  
Sequence 41, Application US/09121952A  
Patent No. 6458355  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc., Hsei, Vanessa  
APPLICANT: Koumenis, Iphigenia  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Shahrokh, Zahra  
APPLICANT: Zapata, Gerardo A.  
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/121.952A  
FILING DATE: 24-Jul-1998  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/074330  
FILING DATE: 22-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/075467  
FILING DATE: 20-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085R4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 729 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
US-09-121-952A-41

Query Match 72.1%; Score 519.2; DB 4; Length 729;  
Best Local Similarity 86.7%; Pred. No. 4.4e-144;  
Matches 572; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCTCCATCACACCTGGAGAGCGGCTCC 120  
DB 70 GATATCGTATGACACAGACCACTCTCCCTGCTGTCAGTCTTGGAGATCAGGCTCC 129  
QY 121 ATCTCTGTAGTCTAGTCAAGCTTAAACAGTAATGGAGACACCTTCTGAGTTGG 180  
DB 130 ATCTCTGTAGTCTAGTCAAGCTTGTACAGGCTTGTACAGGTAATGGAAACCTTATTTACATTGG 189

Query Match 72.1%; Score 519.2; DB 3; Length 729;  
Best Local Similarity 86.7%; Pred. No. 4.4e-144;  
Matches 572; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGACCGGCTCC 120  
DB 70 GATATCGTGATGACACAGACACCACTCTCCCTGCCCTGTGAGTCTTGAGATCAGGCTCC 129

QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTCTGAGTTGG 180  
DB 130 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTCTGAGTTGG 189

QY 181 TATCAGCAGAACGAGGCTCAAGCTTCAAGCTTCTGATTAAGGTTTCTAACCGGGAC 240  
DB 190 TACCTGCAGAAAGCAGGCTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGGATTT 249

QY 241 TCTGGGTTCCAGACAGATTCAGGGCAGTGGGGCAGGACAGATTTTCACACTGAAATC 300  
DB 250 TCTGGGTTCCAGACAGATTCAGGGCAGTGGGGCAGGACAGATTTTCACACTGAAATC 309

QY 301 AGGCGAGTGGAGCTCAAGATTTGGGTTTATTTCTCGGCGAAGGTACAAGACTCCT 360  
DB 310 AGCAGAGTGGAGCTGAGATCTGGGACTTTATTTCTGCTCTCAAGGTACACATGTTCCG 369

QY 361 CCCACTTTCCGGGAGGAGCAAGGTGGAAATCAACGCTACGCTGGCTGCACATCTGTC 420  
DB 370 CTACAGTTGGTGTGGACCAAGCTGGAGCTGAAACGGGCTGTTGCTGCACCACTGTA 429

QY 421 TTCATCTTCCGCTCTGATGAGCAATTTGAAATCTGGAATCTGCCCTCTGTTGTGCTG 480  
DB 430 TTCATCTTCCGCTCTGATGAGCAATTTGAAATCTGGAATCTGCCCTCTGTTGTGCTG 489

QY 481 CTGAATAACTTCTATCCAGAGAGGCTACAGAGCAGGACAGCAAGCTACAGCCTC 540  
DB 490 CTGAATAACTTCTATCCAGAGAGGCTACAGAGCAGGACAGCAAGCTACAGCCTC 549

QY 541 TCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAAGCTACAGCCTC 600  
DB 550 TCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAAGCTACAGCCTC 609

QY 601 AGCAGCACCCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTTTACGCTGCGAA 660  
DB 610 AGCAGCACCCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTTTACGCTGCGAA 669

QY 661 GTCAACCATCAGGGCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGAGGTGTTAA 720  
DB 670 GTCAACCATCAGGGCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGAGGTGTTAA 729

RESULT 8  
US-08-804-444A-41  
; Sequence 41, Application US/08804444A  
; Patent No. 6117980  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania N  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,444A

; FILING DATE: 21-Feb-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 729 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; US-08-804-444A-41

Query Match 72.1%; Score 519.2; DB 3; Length 729;  
Best Local Similarity 86.7%; Pred. No. 4.4e-144;  
Matches 572; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 61 GAAGTTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGACCGGCTCC 120  
DB 70 GATATCGTGATGACACAGACACCACTCTCCCTGCCCTGTGAGTCTTGAGATCAGGCTCC 129

QY 121 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTCTGAGTTGG 180  
DB 130 ATCTCTGTAGTCTAGTCAAGCCTTAAACACAGTAATGGAGACACCTTCTCTGAGTTGG 189

QY 181 TATCAGCAGAACGAGGCTCAAGCTTCAAGCTTCTGATTAAGGTTTCTAACCGGGAC 240  
DB 190 TACCTGCAGAAAGCAGGCTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGGATTT 249

QY 241 TCTGGGTTCCAGACAGATTCAGGGCAGTGGGGCAGGACAGATTTTCACACTGAAATC 300  
DB 250 TCTGGGTTCCAGACAGATTCAGGGCAGTGGGGCAGGACAGATTTTCACACTGAAATC 309

QY 301 AGGCGAGTGGAGCTCAAGATTTGGGTTTATTTCTCGGCGAAGGTACAAGACTCCT 360  
DB 310 AGCAGAGTGGAGCTGAGATCTGGGACTTTATTTCTGCTCTCAAGGTACACATGTTCCG 369

QY 361 CCCACTTTCCGGGAGGAGCAAGGTGGAAATCAACGTAACGGTGGCTGCACCATCTGTC 420  
DB 370 CTACAGTTGGTGTGGACCAAGCTGGAGCTGAAACGGGCTGTTGCTGCACCACTGTA 429

QY 421 TTCATCTTCCGCTCTGATGAGCAATTTGAAATCTGGAATCTGCCCTCTGTTGTGCTG 480  
DB 430 TTCATCTTCCGCTCTGATGAGCAATTTGAAATCTGGAATCTGCCCTCTGTTGTGCTG 489

QY 481 CTGAATAACTTCTATCCAGAGAGGCTACAGAGCAGGACAGCAAGCTACAGCCTC 540  
DB 490 CTGAATAACTTCTATCCAGAGAGGCTACAGAGCAGGACAGCAAGCTACAGCCTC 549

QY 541 TCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAAGCTACAGCCTC 600  
DB 550 TCGGGTAACTCCAGAGAGTGTACAGAGCAGGACAGCAAGCTACAGCCTC 609

QY 601 AGCAGCACCCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTTTACGCTGCGAA 660  
DB 610 AGCAGCACCCTGAGCTGAGCAAGCAGACTACGAGAAACACAAAGTTTACGCTGCGAA 669

QY 661 GTCAACCATCAGGGCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGAGGTGTTAA 720  
DB 670 GTCAACCATCAGGGCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGAGGTGTTAA 729

RESULT 9  
US-09-026-985-41  
; Sequence 41, Application US/09026985  
; Patent No. 6133426  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.

RESULT 6  
US-08-491-334A-55  
; Sequence 55, Application US/08491334A  
; Patent No. 5874080  
; GENERAL INFORMATION:  
; APPLICANT: Hebert, Caroline A.  
; APPLICANT: Kabakoff, Rhona C.  
; APPLICANT: Moore, Mark W.  
; TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory  
; TITLE OF INVENTION: Disorders and Asthma  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/491,334A  
; FILING DATE: 27-Jun-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/398611  
; FILING DATE: 01-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0874P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5530  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 729 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; US-08-491-334A-55

Query Match 72.1%; Score 519.2; DB 2; Length 729;  
Best Local Similarity 86.7%; Pred. No. 4.4e-144;  
Matches 572; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 61 GAAGTTGTGATGACTAGTCTCCACTGTCTCCCTTCCCATCACCTCGAGCGCGCTCC 120  
DB 70 GATATCGTGTGATGACACAGACACACTCTCCCTCGCTGTGATCTTGAGATCAGGCTCC 129  
QY 121 ATCTCTGTAGTCTAGTCAAGCCCTTAAACACAGTAATGGAGACACCTTCTCTAGTTGG 180  
DB 130 ATCTCTGACATCTAGTCAAGCCCTGTACACGGTATTGGAAACACCTATTATACATTGG 189  
QY 181 TATCAGCAGAGCAGCCCACTCAAGCTCTCTGATTTATAGTTTCTTAACCGGAC 240  
DB 190 TACTTGAGAGCCAGCCCACTCTCAAGCTCTCTGATCTCAAAAGTTTCCAACCGATT 249  
QY 241 TCTGGGTCCACAGACATTCACGGCGAGTGGGGCAGGACAGATTTACACTGAAATC 300  
DB 250 TCTGGGTCCACAGACATTCACGGCGAGTGGATCAGGACAGATTTACACTCAGGATC 309  
QY 301 AGCGCAGTGGAGCTGAAGATGTTGGGTTTATTTCTGGGGCAAGGTACAAGGACTCT 360  
DB 310 AGCAGAGTGGAGCTGAGGATCTGGGACTTTATTTCTGTCTCAAAAGTACATGTTCCG 369

RESULT 7

US-09-027-449-41  
; Sequence 41, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027,449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,664  
; FILING DATE: 21-Feb-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 729 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; US-09-027-449-41

US-08-398-611A-55

Query Match	72.1%	Score 519.2	DB 1	Length 729
Best Local Similarity	86.1%	Prod. No. 4.4e-144		
Matches 572	Conservative 0	Mismatches 88	Indels 0	Gaps 0
QY	61	GAAGTGTGATCACTCAAGTCTCCACTGTCCCTTCCCATCACACTGGAGAGCCGGCTCC	120	
DB	70	GATATCGTGATGACACAGACACCACTCTCCCTGCCGTGAGTCTTGGAGATCAGGCGCTCC	129	
QY	121	ATCTCTGTAGTGTCTAGTCAAGGCTTAAACACAGTAAATGGAGACACTTCTTGAGTTGG	180	
DB	130	ATCTCTTGAGATCTAGTCAGGCTTGTACGGTATTTGGAACACTTATTTACATTTGG	189	
QY	181	TATCAGCAAGACCGAGGCCAACTTCCAAAGCTCTGATTTATTAAGGTTTCTAAACCGGAC	240	
DB	190	TACCTGCAAGACCGAGGCCAGTCTCCAAAGCTCTGATCTCAAAGTTTCCAAACCGATT	249	
QY	241	TCTGGGTTCCACAGACAGATTCAGCGGCACTGGGGCAGGACAGATTTTCACTGAAAAATC	300	
DB	250	TCTGGGTTCCACAGACAGTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAGGATC	309	
QY	301	AGCGCAGTGGAGGCTGAAGATGTTGGGTTTATTTCTGGGGCAGGTACAAGGACTCTCT	360	
DB	310	AGCAGTGGAGGCTGAGGATCTGGGACTTTATTTCTGCTCTCAAAGTACACATGTTTCCG	369	
QY	361	CCACATTTCCGCGGAGGACCAAGGTGGAAATCAAAACGTACGGTGGCTGCACCATCTGC	420	
DB	370	CTCAGTTCCGTTCTGGGACCAAGCTGGAGCTGAAACGGGCTGTTGCTGCACCACTGA	429	
QY	421	TTTCATTTCCGCCCATCTGATGAGCAGTTGAAATCTGGAACTGCTCTGTGTGTCGCTG	480	
DB	430	TTTCATTTCCCAACCATCCAGTGAGCAATTGAAATCTGGAACTGCTCTGTGTGTCGCTG	489	
QY	481	CTGAATAACTTCTATTCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATTAACGCCCTCCAA	540	
DB	490	CTGAATAACTTCTATTCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATTAACGCCCTCCAA	549	
QY	541	TCCGGTTAACTCCCAAGGAGTGTACAGAGCAGGACAGCAAGGACAGCACTTACAGCCTC	600	
DB	550	TCCGGTTAACTCCCAAGGAGTGTACAGAGCAGGACAGCAAGGACAGCACTTACAGCCTC	609	
QY	601	AGCAGACCCCTGAGCCTGAGCAAGCAGACTACGAAACACAAAGTCTAGCGCTCGGAA	660	
DB	610	AGCAGACCCCTGAGCCTGAGCAAGCAGACTACGAAACACAAAGTCTAGCGCTCGGAA	669	
QY	661	GTCACCCATCAGGGCCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGAGAGTGTGA	720	
DB	670	GTCACCCATCAGGGCCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGAGAGTGTGA	729	

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RESULT 5
US-08-396-851A-55
; Sequence 55, Application US/08396851A
; Patent No. 5707622
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk.
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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Best Local Similarity 100.0%; Pred. No. 2e-203; 0; Gaps 0;  
Matches 720; Conservative 0; Mismatches 0; Indels 0;

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Db 1 ATGAGCCTCCCTGCTCAGCTCCTCGGCTCTATTGCTCTGCTCCCGGTCAGTGG 60

Qy 61 GAAGTTGTGATGACTGACTGCTCAGCTGCTCCCTTCCCATCAGCTGGAGAGCGGCTCC 120  
Db 61 GAAGTTGTGATGACTGACTGCTCAGCTGCTCCCTTCCCATCAGCTGGAGAGCGGCTCC 120

Qy 121 ATCTCCTGTAGTCTAGTCAAGCCTTAAACAGATTAATGGAGACACCTTCTCTGAGTTGG 180  
Db 121 ATCTCCTGTAGTCTAGTCAAGCCTTAAACAGATTAATGGAGACACCTTCTCTGAGTTGG 180

Qy 181 TATCAGCAGAACCCAGGCGCACTTCAAGCTCCTGATTTAATAGTTTCTAACCGGGAC 240  
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Qy 241 TCTGGGGTCCAGACAGATTTCAGGCGAGTGGGCGAGGACAGATTTCACCTGAAATC 300  
Db 241 TCTGGGGTCCAGACAGATTTCAGGCGAGTGGGCGAGGACAGATTTCACCTGAAATC 300

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Db 301 AGCCAGTGGAGGCTGAAGATGTTGGGGTTTATTTCTGGGGCAAGGTACAGGACTCCT 360

Qy 361 CCCACTTTCCGGCGGAGGACCAAGTGGAAATCAAAAGTACGGTGGCTCAGCATCTGTC 420  
Db 361 CCCACTTTCCGGCGGAGGACCAAGTGGAAATCAAAAGTACGGTGGCTCAGCATCTGTC 420

Qy 421 TTCACTTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTCCTG 480  
Db 421 TTCACTTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGCTCTGTTGTCCTG 480

Qy 481 CTGAATTAATCTTATCCAGAGAGGCAAGTACAGTGAAGTGAATACCGCTCCAA 540  
Db 481 CTGAATTAATCTTATCCAGAGAGGCAAGTACAGTGAAGTGAATACCGCTCCAA 540

Qy 541 TCGGGTAATCTCCAGAGAGTGTACAGAGCAGGACAGCAAGGACAGACCTTACAGCTC 600  
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Qy 601 AGCAGACCTTGAGCTGAGCAAGAGACTACGAGAAACACAAAGTCTACCGCTCGAA 660  
Db 601 AGCAGACCTTGAGCTGAGCAAGAGACTACGAGAAACACAAAGTCTACCGCTCGAA 660

Qy 661 GTCAACCATCAGGCGCTGAGCTCGCGTCCAAAGAGCTTCAACAGGGGAGAGTTGA 720  
Db 661 GTCAACCATCAGGCGCTGAGCTCGCGTCCAAAGAGCTTCAACAGGGGAGAGTTGA 720

RESULT 2  
US-08-398-613A-55  
; Sequence 55, Application US/08398613A  
; Patent No. 5677426  
; GENERAL INFORMATION:  
; APPLICANT: Fong, Sherman  
; APPLICANT: Hebert, Caroline Alice  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398,613A  
; FILING DATE: 01-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 874P1-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1489  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 729 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-398-613A-55

Query Match 72.1%; Score 519.2; DB 1; Length 729;

Best Local Similarity 86.7%; Pred. No. 4.4e-144; Indels 0; Gaps 0;

Matches 572; Conservative 0; Mismatches 88;

Qy 61 GAAGTTGTGATGACTGCTCAGTCTCCACTGCTCCCTTCCCATCAGCTGGAGAGCGGCTCC 120  
Db 70 GATATCGTATGACACAGACACCACTCTCCCTGCTGTCAGTCTTGGAGATCAGGCTCC 129

Qy 121 ATCTCCTGTAGTCTAGTCAAGCCTTAAACAGATTAATGGAGACACCTTCTGAGTTGG 180  
Db 130 ATCTCCTGTAGTCTAGTCAAGCCTTAAACAGATTAATGGAGACACCTTCTGAGTTGG 189

Qy 181 TATCAGCAGAACCCAGGCGCAAGTGGAAATCTGGAATCTGGAATCTGGAATCTGGAATCT 240  
Db 190 TACCTCGAGAGCCAGGCGCAGTCTCCAAAGTCTCTGATCTACAAAGTCTTCCAAAGTCT 249

Qy 241 TCTGGGGTCCAGACAGATTTCAGGCGAGTGGGCGAGGACAGATTTCACTGAAATC 300  
Db 250 TCTGGGGTCCAGACAGATTTCAGGCGAGTGGGCGAGGACAGATTTCACTGAAATC 309

Qy 301 AGCGCAGTGGAGGCTGAGATGTTGGGGTTTATTTCTGGGGCAAGGTACAGGACTCCT 360  
Db 310 AGCAGAGTGGAGGCTGAGATGTTGGGGTTTATTTCTGGGGCAAGGTACAGGACTCCT 369

Qy 361 CCACATTTCCGGCGGAGGACCAAGTGGAAATCAAAAGTACGGTGGCTGCAACCTCTCTC 420  
Db 370 CTCACGTTCCGGTCTGGGACCAAGTGGAGCTGAAACCGGCTGTTGCTGCAACCTCTCTA 429

Qy 421 TTCACTTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCTGGAATCTGGAATCTG 480  
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Qy 481 CTGAATAAATCTTCTATCCAGAGAGGCGCAAGTACAGTGGAGGTGGAATAGCGCTCCAA 540  
Db 490 CTGAATAAATCTTCTATCCAGAGAGGCGCAAGTACAGTGGAGGTGGAATAGCGCTCCAA 549

Qy 541 TCGGGTAACTTCCAGAGAGTGTACAGAGCAGGACAGGACAGGACAGCTTACAGCTC 600  
Db 550 TCGGGTAACTTCCAGAGAGTGTACAGAGCAGGACAGGACAGGACAGCTTACAGCTC 609

Qy 601 AGCAGACCTTGAGCTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTACGCTTCCAA 660  
Db 610 AGCAGACCTTGAGCTGAGCAAGAGCAGACTACGAGAAACACAAAGTCTACGCTTCCAA 669

Qy 661 GTCAACCATCAGGCGCTGAGCTCGCGCTCCAAAGAGCTTCAACAGGGGAGAGTTGA 720  
Db 670 GTCAACCATCAGGCGCTGAGCTCGCGCTCCAAAGAGCTTCAACAGGGGAGAGTTGA 729

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Title: US-09-758-173-5

Perfect score: 720

Sequence: 1 ATGAGCTCCTGCTCAGCT.....TCAACAGGGAGAGTGTGA 720

Scoring table: IDENTITY\_NUC

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	519.2	72.1	729	1	US-08-398-613A-55
3	519.2	72.1	729	1	US-08-398-612A-55
4	519.2	72.1	729	1	US-08-398-611A-55
5	519.2	72.1	729	1	US-08-396-851A-55
6	519.2	72.1	729	2	US-08-491-334A-55
7	519.2	72.1	729	3	US-09-027-449-41
8	519.2	72.1	729	3	US-08-804-444A-41
9	519.2	72.1	729	3	US-09-026-985-41
10	519.2	72.1	729	4	US-09-121-952A-41
11	519.2	72.1	729	4	US-09-234-340A-41
12	489.4	68.0	5703	1	US-08-467-420A-50
13	489.4	68.0	5703	1	US-08-470-110A-50
14	489.4	68.0	5703	1	US-08-667-769A-50
15	489.4	68.0	5703	2	US-08-940-371-50
16	489.4	68.0	5703	3	US-08-637-647-50
17	489.4	68.0	5703	5	PCT-US95-17082A-50
18	486.4	67.6	19040	4	US-09-343-485A-3
19	474.8	65.9	931	3	US-09-049-672A-19
20	471.6	65.5	1066	1	US-08-157-101A-4
21	468.8	65.1	705	1	US-08-488-376-16
22	468.8	65.1	705	2	US-08-634-223-16
23	468.8	65.1	705	2	US-08-634-224-16
24	468.8	65.1	705	2	US-08-634-400-16
25	468.8	65.1	705	2	US-08-635-878-16
26	468.8	65.1	705	2	US-08-770-057-16
27	468.8	65.1	705	4	US-09-335-697B-16

28 468.8 65.1 705 4 US-09-335-697B-16 Sequence 16, Appl  
29 462 64.2 729 1 US-08-276-852-152 Sequence 152, App  
30 462 64.2 729 1 US-08-276-852-152 Sequence 152, App  
31 462 64.2 729 1 US-08-899-575-152 Sequence 152, App  
32 462 64.2 729 1 US-08-899-575-152 Sequence 152, App  
33 462 64.2 729 1 US-08-899-575-152 Sequence 152, App  
34 462 64.2 729 1 US-08-899-575-152 Sequence 152, App  
35 462 64.2 729 5 PCT-US95-08743-152 Sequence 152, App  
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45 460.4 63.9 3819 4 US-09-042-353-393 Sequence 393, App

#### ALIGNMENTS

RESULT 1  
US-08-487-550-5  
; Sequence 5, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/487,550  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: 435  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 720 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..720  
; NAME/KEY: mat\_peptide  
; LOCATION: 1..720  
US-08-487-550-5  
Query Match 100.0%; Score 720; DB 3; Length 720;

us-09-758-173-7.rge

Sun Apr 6 09:17:24 2003

Db 1401 GAGGCTCTGCACAAACCACTACACGACAGAGAGCCTCTCCCTGTCTCTCCGGGTAAATGA 1457

Search completed: April 6, 2003, 01:56:13  
Job time : 4520.08 secs



Query Match	81.5%	Score 1171.8	DB 9	Length 3143
Best Local Similarity	89.8%	Prod. No. 26-227		
Matches 1283	Conservative	Mismatches 137	Indels	Gaps 2

  

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Db	73	ATGGAGTTTGGGCTGAGCTGGTCTTCTCGTTGCTCTTTAAGAGGTGTCAGTGTCTAG	132
Qy	61	GTGCACACTGGTGGAGTCTGGGGGAGGCTTGCTCCAGCCTGGCGGGTCCCTGAGAGTCTCC	120
Db	133	GGCGAGTTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCCGGGAGCTCCCTGAGACTCTCC	192
Qy	121	TGTGCAGTCTCTGGATTCCACTTCAGTGCACCACTACATGATTGGTTCCGCCAGGCTCCA	180
Db	193	TGTGCAGCCTCTGGTTTCAGGTTTCAGCAATTATGGCATGCACCTGGGTCGCCAGGCTCCA	252
Qy	181	GGGAAGGGCCCGGAATGGTAGGTTTCATTAGAAACAAACCGAACGGTGGGACACAGAA	240
Db	253	GGCAAGGGGCTGGAGTGGGGTGGCAGTTTTTTCATATGATGAAGTCAAT-----AAATAT	306
Qy	241	TACGCCGGGCTCTGTGAAGAAGACAGATTCACCATCTCCAGAGATGATTCAAAGACATCGCC	300
Db	307	TATGCAGCCTCCGTGAAGGTCGATTACCATCTCCAGAGACAACTCCAGAACACGTTG	366
Qy	301	TATCTGCAANTGAGCAGCCTGAAATCGAGGACACGGCCGTCTATTCTGTACTACATCC	360
Db	367	TCTCTGCAAAATGAACAGCCTGAGAGTTTGAGGACACGGCTGTTTACTGTCTGCGAAAGAT	426
Qy	361	TACATTTTACATTTGTCGGGGTGGTGTCTGCTATGAGAGGTTACTTCGAATTTCTGGGGCCAG	420
Db	427	CAGAAAGCCCTGCTACAGCAACAG--CTGGTTCTTAACCAACTTTGACTCTTGGGCGGG	483
Qy	421	GGGGCCCTGGTCAAGGTCCTCGTCTAGCACAAAGGGCCCATCGGTCTTCCCTCTGGCA	480
Db	484	GGCACCTTGGTACCGTCTCTCAGCCTCACCAAGGGGCCCATCGGTCTTCCCTCTGGCA	543
Qy	481	CGCTCCTCAAGAGACACTCTTGGGGGACACAGCGGCCCTCGGGTGTCTGTCAAGGACTAC	540
Db	544	CCCTCTCCAAGAGACACTCTTGGGGGACACAGCGGCCCTGGGCTGCTTGTCAAGGACTAC	603
Qy	541	TTTCCCGGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACACAGCGGCGTGCACACC	600
Db	604	TTTCCCGGAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACACAGGGGCGTGCACACC	663
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RESULT 15	HS1GG1:KHK	1624 bp	mrna	linear	PRI 19-AUG-1998
LOCUS	HS1GG1:KHK				
DEFINITION	Homo sapiens mRNA for immunoglobulin kappa heavy chain.				
ACCESSION	Y14735				
VERSION	Y14735.1	GI:2765420			
KEYWORDS	constant region; IG1; immunoglobulin; kappa heavy chain; variable region.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1624)				
AUTHORS	Paterson,T., Innes,J., McMillan,L., Downing,I. and Carter,M.C.				
TITLE	Variation in IG1 heavy chain allotype does not contribute to differences in biological activity of two human anti-Rhesus (D) monoclonal antibodies				
JOURNAL	Immunotechnology 4 (1), 37-47 (1998)				

[illegible]

Location/Qualifiers

Db 260 GGAAGGGCTCGAGTGGG-----TCTCAAGTATTACTGCCAGTGGTGAAGACATAC 313  
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 Db 314 GAGCGAGACTTCTGTAAGGGCGGTTCACCATCTCCAGAGACAATTCAGGAACACTCTG 373  
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 Qy 841 ACCTCATGATCTCCGGACCCCTGAGGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
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 Qy 1381 GAGGCTCTGCAACAACCTACACGAGGAGGAGCTTCTCTCTGCTCTCCGGGTAAATGA 1437  
 Db 1442 GAGGCTCTGCAACAACCTACACGAGGAGGAGCTTCTCTCTGCTCTCCGGGTAAATGA 1498  
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 LOCUS Homo sapiens cDNA FLJ39691 fis, clone SMINT2010672, highly similar  
 DEFINITION to Homo sapiens mRNA for immunoglobulin lambda heavy chain.  
 AK097010  
 ACCESSION  
 VERSION AK097010.1 GI:21756642  
 KEYWORDS oligo capping; fis (full insert sequence).  
 SOURCE Homo sapiens small intestine cDNA to mRNA, clone\_lib:SMINT2  
 clone:SMINT2010672.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,  
 Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R.,  
 Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,  
 Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,  
 Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,  
 Watanabe, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,  
 Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,  
 Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.  
 NEDO human cDNA sequencing project  
 TITLE Unpublished  
 JOURNAL 2 (bases 1 to 1631)  
 REFERENCE Isogai, T. and Yamamoto, J.  
 AUTHORS Direct Submission  
 TITLE Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7  
 JOURNAL Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan  
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 COMMENT NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;  
 Research Association for Biotechnology (RAB); cDNA library  
 construction; Helix Research Institute (HRI) (supported by Japan  
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing; RAB,  
 HRI, and Biotechnology Center, National Institute of Technology and  
 Evaluation; clone selection for full insert sequencing; HRI and  
 RAB; annotation: HRI and RAB.  
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Db 1389: TACAGCAAGCTCACCCTGACACAGCAGGTGGCAGAGGAGGAGCTTCTTCATGCTCC 1448

Qy 1372 GTGATGATGAGGCTCTGCAACACCTACACGCAAGAGCCTCTCCCTGTCTCCGGGT 1431  
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Qy 1432 AATGA 1437  
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Db 1509 AATGA 1514

RESULT 6

LOCUS BC018747 1679 bp mRNA linear PRI 11-DEC-2001

DEFINITION Homo sapiens, Similar to immunoglobulin heavy constant gamma 3 (G3m marker), clone MGC:31937 IMAGE:4851063, mRNA, complete cds.

ACCESSION BC018747

VERSION BC018747.1 GI:17511791

KEYWORDS MGC.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 1679)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk  
Email: [cgapps-r@mail.nih.gov](mailto:cgapps-r@mail.nih.gov)  
Tissue Procurement: Louis Staudt  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 40 Row: 1 Column: 16  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction, Similarity but not identity to protein.

FEATURES

source

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BASE COUNT 430 a 506 c 452 g 291 t

ORIGIN

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Best Local Similarity 90.5%; Pred. No. 9.9e-231;  
Matches 1300; Conservative 0; Mismatches 113; Indels 24; Gaps 2;

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FEATURES  
SOURCE

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BASE CO  
OPTICN

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:13:05 ; Search time 4509.08 Seconds  
(without alignments)  
9274.790 Million cell updates/sec

Title: US-09-758-173-7

Perfect score: 1437

Sequence: 1 ATGGGTGGAGCCTCATCTT.....CCCTCTCTCCGGTAAATGA 1437

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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GenEmbl.\*

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
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20: em\_om.\*  
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37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1437	100.0	1437	6	AR108865	Sequence
2	1238.6	86.2	1642	9	AK093806	Homo sapi
3	1219	84.8	7521	6	AX080951	Sequence
4	1208	84.1	1659	9	BC014667	Homo sapi
5	1189.2	82.8	1666	9	BC006402	Homo sapi
6	1188.2	82.7	1679	9	BC018747	Homo sapi
7	1186.2	82.5	1630	9	BC024289	Homo sapi
8	1185	82.5	1430	6	AX419496	Sequence
9	1184.6	82.4	1549	6	A21385	plasmid DNA
10	1184	82.4	1673	9	HSIGG1LH	Homo sapien
11	1183.4	82.4	1633	9	AK097859	Homo sapi
12	1182.2	82.3	1990	9	AK098817	Homo sapi
13	1173	81.6	1631	9	AK097010	Homo sapi
14	1171.8	81.5	3143	9	BC019046	Homo sapi
15	1169.4	81.4	1624	9	HSIGG1KH	Homo sapien
16	1166.6	81.2	1633	9	AK097367	Homo sapi
17	1162.2	80.9	1419	12	AF019036	Synthetic
18	1155	80.4	1627	9	AK097350	Homo sapi
19	1155	80.4	1639	9	AK097350	Homo sapi
20	1148.2	79.9	1624	9	AK097206	Homo sapi
21	1147.2	79.8	1335	6	AX010615	Sequence
22	1147.2	79.8	1335	6	AX010646	Sequence
23	1141.4	79.4	1620	9	AK097366	Homo sapi
24	1140	79.3	1353	6	AX277242	Sequence
25	1139.8	79.3	1618	9	AK097360	Homo sapi
26	1138.6	79.2	1637	9	AK093636	Homo sapi
27	1133.4	78.9	1599	6	AX130501	Sequence
28	1133.4	78.9	1599	6	AX133307	Sequence
29	1133.4	78.9	1599	6	AX334122	Sequence
30	1133.4	78.9	1599	9	HUMIGHEPAH	Human (hybr
31	1132	78.8	1401	9	AF027159	Homo sapi
32	1131.8	78.8	1617	6	A29585	H. sapiens c
33	1127.4	78.5	1622	9	AK097359	Homo sapi
34	1127.4	78.5	9209	6	AR000007	Sequence
35	1127.4	78.5	9209	6	AR015961	Sequence
36	1127.4	78.5	9209	6	AR060920	Sequence
37	1127.4	78.5	9209	6	AR211052	Sequence
38	1127.4	78.5	9209	6	AX032414	Sequence
39	1127.4	78.5	9209	6	BD004714	Chimeric
40	1127.4	78.5	18986	6	AR051652	Sequence
41	1127.4	78.5	18986	6	AR092290	Sequence
42	1126.2	78.4	1465	10	S79307	IG gamma =i
43	1120.6	78.0	1404	6	AX268679	Sequence
44	1120.6	78.0	8120	6	AR116673	Sequence
45	1120.4	78.0	1628	9	AK097361	Homo sapi

# ALIGNMENTS

RESULT 1  
AR108865  
LOCUS AR108865 1437 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 7 from patent US 6113898.  
ACCESSION AR108865  
VERSION AR108865.1 GI:12825141  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 1437)  
Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.  
Human B7.1-specific primatized antibodies and transfectomas  
expressing said antibodies  
Patent: US 6113898-A 7 05-SEP-2000;  
JOURNAL

Pred. No. is the number of results predicted by chance to have a

Db 144 FIFPPSDEQLKSGTASVVCVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 203  
Qy 201 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 239  
Db 204 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 242

RESULT 15  
US-09-026-985-62  
; Sequence 62, Application US/09026985  
; Patent No. 6133426  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,985  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-026-985-62

Query Match 75.4%; Score 936; DB 4; Length 242;  
Best Local Similarity 81.7%; Pred. No. 1.8e-74;  
Matches 179; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

Qy 21 EVVMTQSPSLSLPTTPGEPASISCRSSQSLKHSNGDTFLSWYQKQKQPPLLIYKVSNRD 80  
Db 24 DIQMTQSPSSLSASVGRVITTCRSSQSLVHGIGETYLHWYQKQKGPAPKLLIYKVSNR 83  
Qy 81 SGVPRFSGSGAGTDFTLKISAVEADGVYFCGQGTPTPTFGGKVEIKRTVAAPSV 140  
Db 84 SGVPRFSGSGAGTDFTLTSSQPEDFATYCSQSTHVPLTFPGQKVEIKRTVAAPSV 143  
Qy 141 FIFPPSDEQLKSGTASVVCVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200  
Db 144 FIFPPSDEQLKSGTASVVCVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 203  
Qy 201 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 239  
Db 204 SSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 242

Search completed: March 29, 2003, 09:17:41  
Job time : 8.49182 secs

Db 61 WYQKQPPKLLIFWASTRESGVDPFRFSGSGFGDTFTLTSSLAQADVAVYCOQYFSY 120  
 QY 120 PPFPGGKTKVEIKRTVAAPSVFIFFPSDBQLSGTASVVCLLNPFYPREAKVQWKVDNAL 179  
 Db 121 PLTFGGGKTKVEIKRTVAAPSVFIFFPSDBQLSGTASVVCLLNPFYPREAKVQWKVDNAL 180  
 QY 180 QSGNSQSVTEQSDKSTYSLSTLTLSKADYKHKVACEVTHOGLSSPVTYKSNRGE 239  
 Db 181 QSGNSQSVTEQSDKSTYSLSTLTLSKADYKHKVACEVTHOGLSSPVTYKSNRGE 240

## RESULT 13

US-09-049-672A-6  
 ; Sequence 6, Application US/09049672A  
 ; Patent No. 6135941  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Yue, Henry  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Corley, Neil C.  
 ; APPLICANT: Guegler, Karl J.  
 ; APPLICANT: Baughn, Mariah R.  
 ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/049,672A  
 FILING DATE: HEREWITH  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cerrione, Michael C  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0497 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 TELEX:

INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 234 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: COLSUCT01  
 CLONE: 2280869  
 US-09-049-672A-6

Query Match 75.6%; Score 939.5; DB 4; Length 234;  
 Best Local Similarity 77.0%; Pred. No. 8.3e-75;  
 Matches 184; Conservative 23; Mismatches 27; Indels 5; Gaps 2;

QY 1 MSPLAQLGLLLLCVPGSSGEVMTQSPLSLPTTEPEPASISCRSSQSLKHSNGDTFLSW 60  
 Db 1 MEAPQALLFLLLLPDSFGIEIWMQSPAIVSLSPGERATLSCRASQSI----GST-IAW 55

QY 61 YQKQGPRLLIYKVSNRDGSVDPFRFSGSGAGTDTFTLKISAVEAEADVGVYFCQGT RTP 120  
 Db 56 YQRRQGPRLLIYGASTRATGVPFRFSGSGGTFTFTLFISSLOSEDFALYYCOQYKGP 115  
 QY 121 PTFGGGKTKVEIKRTVAAPSVFIFFPSDBQLSGTASVVCLLNPFYPREAKVQWKVDNALQ 180  
 Db 116 LTFGGGTRVQIIRTVAAAPSVFIFFPSDBQLSGTASVVCLLNPFYPREAKVQWKVDNALQ 175  
 QY 181 SGNSESQSVTEQSDKSTYSLSTLTLSKADYKHKVACEVTHOGLSSPVTYKSNRGE 239  
 Db 176 SGNSESQSVTEQSDKSTYSLSTLTLSKADYKHKVACEVTHOGLSSPVTYKSNRGE 234

## RESULT 14

US-09-027-449-62  
 ; Sequence 62, Application US/09027449  
 ; Patent No. 6025158  
 ; GENERAL INFORMATION:

APPLICANT: Gonzalez, Tania R.  
 APPLICANT: Leong, Steven R.  
 APPLICANT: Prebica, Leonard G.  
 TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
 TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/027,449  
 FILING DATE: 20-Feb-1998  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/074,330  
 FILING DATE: 22-Jan-1998  
 PRIOR APPLICATION DATA: 60/038,664  
 FILING DATE: 21-Feb-1997  
 ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.  
 REGISTRATION NUMBER: 34,659  
 REFERENCE/DOCKET NUMBER: P1085R3-2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-5530  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 62:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 242 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear

US-09-027-449-62  
 Query Match 75.4%; Score 936; DB 3; Length 242;  
 Best Local Similarity 81.7%; Pred. No. 1.8e-74;  
 Matches 179; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 21 EVVMTQSPLSLPTTEPEPASISCRSSQSLKHSNGDTFLSWYQKQGPRLLIYKVSNRD 80  
 Db 24 DIQMTQSPSSLSASVGRVTITCRSSQSLVHGIGETVLYHWYQKQPGKAPKLLIYKVSNR 83  
 QY 81 SGVDPFRFSGSGAGTDTFTLKISAVEAEADVGVYFCQGT RTPPTFTFGGKTKVEIKRTVAAPSV 140  
 Db 84 SGVDPFRFSGSGAGTDTFTLTSSLPEDFATYCYCSQSTHVLPTFTGQGTKEIKRTVAAPSV 143  
 QY 141 FTFPPSDQLSGTASVVCLLNPFYPREAKVQWKVDNALQSGNSQSVTEQSDKSTYSL 200

APPLICATION NUMBER: 60/075467  
FILING DATE: 20-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085R4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 242 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-121-952A-42

Query Match 78.6%; Score 976; DB 4; Length 242;  
Best Local Similarity 84.5%; Pred. No. 5.6e-78;  
Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 21 EVVMTQSPPLSPITGCEPASISCRSSQSLKHSNGDTFLSWYQKQGPPLLIYKVSNRD 80  
DB 24 DIVMTQTPLSPVSLGDAQISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNR 83  
QY 81 SGVPRFSGSGAGTDTFLKISAVEAEDVGVIYFCGQGTPTPTFGGKVEIKRTVAAPSV 140  
DB 84 SGVPRFSGSGGTDTFLIRSRVEAEDLGLYFCQSOSTHVPLTFGAGTKLEKRAVAAPT 143  
QY 141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKQVQVDNALQSGNSQESVTEQDSKDYSL 200  
DB 144 FIFPPSSEQLKSGTASVVCLLNNFYPREAKQVQVDNALQSGNSQESVTEQDSKDYSL 203  
QY 201 SSTLTLSKADYKHKYKVIYACEVTHQGLSSPVTKSFNRGEC 239  
DB 204 SSTLTLSKADYKHKYKVIYACEVTHQGLSSPVTKSFNRGEC 242

RESULT 11  
US-09-234-340A-42  
Sequence 42, Application US/09234340A  
Patent No. 6468532  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc., Hsui, Vanessa  
APPLICANT: Koumenis, Inphigenia  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Shahrokh, Zahra  
APPLICANT: Zapata, Gerardo A.  
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/234,340A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/121,952  
FILING DATE: 24-Jul-1998  
APPLICATION NUMBER: 60/074330  
FILING DATE: 22-JAN-1998  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/075467  
FILING DATE: 20-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085R4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 242 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-234-340A-42

Query Match 78.6%; Score 976; DB 4; Length 242;  
Best Local Similarity 84.5%; Pred. No. 5.6e-78;  
Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 21 EVVMTQSPPLSPITGCEPASISCRSSQSLKHSNGDTFLSWYQKQGPPLLIYKVSNRD 80  
DB 24 DIVMTQTPLSPVSLGDAQISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNR 83  
QY 81 SGVPRFSGSGAGTDTFLKISAVEAEDVGVIYFCGQGTPTPTFGGKVEIKRTVAAPSV 140  
DB 84 SGVPRFSGSGGTDTFLIRSRVEAEDLGLYFCQSOSTHVPLTFGAGTKLEKRAVAAPT 143  
QY 141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKQVQVDNALQSGNSQESVTEQDSKDYSL 200  
DB 144 FIFPPSSEQLKSGTASVVCLLNNFYPREAKQVQVDNALQSGNSQESVTEQDSKDYSL 203  
QY 201 SSTLTLSKADYKHKYKVIYACEVTHQGLSSPVTKSFNRGEC 239  
DB 204 SSTLTLSKADYKHKYKVIYACEVTHQGLSSPVTKSFNRGEC 242

RESULT 12  
US-09-301-593-36  
Sequence 36, Application US/09301593A  
Patent No. 6455677  
GENERAL INFORMATION:  
APPLICANT: Park, John E.  
APPLICANT: Garin-Chesa, Pilar  
APPLICANT: Bamberger, Uwe  
APPLICANT: Legier, Olivier  
APPLICANT: Saidanna, Jose W.  
APPLICANT: Rettig, Wolfgang J.  
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
FILE REFERENCE: 0652.1890001  
CURRENT APPLICATION NUMBER: US/09/301,593A  
CURRENT FILING DATE: 1999-04-29  
EARLIER APPLICATION NUMBER: EP 98107925.4  
EARLIER FILING DATE: 1998-04-30  
EARLIER APPLICATION NUMBER: US 60/086,049  
EARLIER FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 240  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-301-593-36

Query Match 78.5%; Score 975.5; DB 4; Length 240;  
Best Local Similarity 80.4%; Pred. No. 6.1e-78;  
Matches 193; Conservative 18; Mismatches 28; Indels 1; Gaps 1;

QY 1 MSLPAQLLLGLLILCVPGSGEVVMTQSPPLSPITGCEPASISCRSSQSLKHS-NGDTFLS 59  
DB 1 METDTLLWVLLWVPGSSGDIWMTQSPDLSAVSLGERATINCKSSQSLIYSRNQNYLA 60  
QY 60 WYQKPGQPPRLIYKVSNRDVGVPDRFSGAGTDTFLKISAVEAEDVGVIYFCGQGT 119







Qy 201 SSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSNRGE 239  
Db 204 SSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSNRGE 242

RESULT 4  
US-08-398-612A-56  
; Sequence 56, Application US/08398612A  
; Patent No. 5686070  
; GENERAL INFORMATION:  
; APPLICANT: Doershuk, Claire M.  
; APPLICANT: Fong, Sherman  
; APPLICANT: Hebert, Caroline Alice  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for  
; TREATMENT OF INFLAMMATORY DISORDERS  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398,612A  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/398611  
; FILING DATE: 01-MAR-1995  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0874P1  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-398-612A-56

Query Match 78.6%; Score 976; DB 1; Length 242;  
Best Local Similarity 84.5%; Pred. No. 5.6e-78;  
Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;  
Qy 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPRLLIYKVSNRD 80  
Db 24 DIVMTQPLSLPVLGDAQSISCRSSQSLVHGIGNTYLVHWYLPKPGQSPKLLIYKVSNR 83  
Qy 81 SGVPDRFSGSGAGTDFTLTKISAVEAEADVGVYFCQGTRTPPTFGGKTKVEIKRTVAAPSV 140  
Db 84 SGVPDRFSGSGAGTDFTLTKISAVEAEADVGVYFCQSTHPLTFGAGTKLEKRAVAAPT 143  
Qy 141 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 200  
Db 144 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 203  
Qy 201 SSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSNRGE 239

US-08-491-334A-56  
RESULT 6  
US-08-491-334A-56

Db 204 SSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSNRGE 242

RESULT 5  
US-08-398-611A-56  
; Sequence 56, Application US/08398611A  
; Patent No. 5702946  
; GENERAL INFORMATION:  
; APPLICANT: Doershuk, Claire M.  
; APPLICANT: Fong, Sherman  
; APPLICANT: Hebert, Caroline Alice  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment  
; OF INFLAMMATORY DISORDERS  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398,611A  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0874P1  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-398-611A-56

Query Match 78.6%; Score 976; DB 1; Length 242;  
Best Local Similarity 84.5%; Pred. No. 5.6e-78;  
Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;  
Qy 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPRLLIYKVSNRD 80  
Db 24 DIVMTQPLSLPVLGDAQSISCRSSQSLVHGIGNTYLVHWYLPKPGQSPKLLIYKVSNR 83  
Qy 81 SGVPDRFSGSGAGTDFTLTKISAVEAEADVGVYFCQGTRTPPTFGGKTKVEIKRTVAAPSV 140  
Db 84 SGVPDRFSGSGAGTDFTLTKISAVEAEADVGVYFCQSTHPLTFGAGTKLEKRAVAAPT 143  
Qy 141 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 200  
Db 144 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 203  
Qy 201 SSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSNRGE 239  
Db 204 SSTLTLSKADYEHKHYVACEVTHQGLSSPVTKSNRGE 242

RESULT 6  
US-08-491-334A-56

QY 61 YQOKPGOPRLLIYKVSNDSCVPRDFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRP 120  
Db 61 YQOKPGOPRLLIYKVSNDSCVPRDFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRP 120  
QY 121 PTFGGKTVEIKRTVAAPSVFIIPPSPDQKSGTASVVCLNNFYPREAKVQWKVDNALQ 180  
Db 121 PTFGGKTVEIKRTVAAPSVFIIPPSPDQKSGTASVVCLNNFYPREAKVQWKVDNALQ 180  
QY 181 SGNQSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239  
Db 181 SGNQSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239

## RESULT 2

US-07-916-098A-56  
; Sequence 56, Application US/07916098A  
; Patent No. 5871732  
; GENERAL INFORMATION:  
; APPLICANT: BURKLY, LINDA C.  
; APPLICANT: CHISHOLM, PATRICIA L.  
; APPLICANT: THOMAS, DAVID W.  
; APPLICANT: ROSA, MARGARET D.  
; APPLICANT: ROSA, JOSEPH J.  
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
; TREATMENT OF AIDS, ARC AND HIV INFECTION  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
; STREET: 10 SOUTH WACKER DRIVE  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: U.S.A.  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07916.098A  
; FILING DATE: July 24, 1992  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/08843  
; FILING DATE: No. 5871732ember 27, 1991  
; CLASSIFICATION: 424  
; APPLICATION NUMBER: 07/618,542  
; FILING DATE: No. 5871732ember 27, 1990  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: JOHN J. MC DONNELL  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 92,310-G  
; TELEPHONE: (312) 715-1000  
; TELEFAX: (312) 715-1234  
; TELEX: 910/221-5317  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-916-098A-56

Query Match 78.7%; Score 978; DB 2; Length 241;  
Best Local Similarity 80.4%; Pred. No. 3.7e-78;  
Matches 193; Conservative 22; Mismatches 23; Indels 2; Gaps 2;  
QY 1 MSIPAGLLGLLLICVPGSGEVMTQSPLSLPITPGEPASISCRSSQSLKHS-NGDTFLS 59  
Db 3 MRVPAQLGLLLWLPFGAGDIVMTQSPDLSAVSLGERATINCKSSGLLYSTINQNYLA 62

QY 60 WYQOKPGOPRLLIYKVSNDSCVPRDFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRT 119  
Db 63 WYQOKPGOPRLLIYKVSNDSCVPRDFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRT 121  
QY 120 PTFGGKTVEIKRTVAAPSVFIIPPSPDQKSGTASVVCLNNFYPREAKVQWKVDNAL 179  
Db 122 YRTFGGKTVEIKRTVAAPSVFIIPPSPDQKSGTASVVCLNNFYPREAKVQWKVDNAL 181  
QY 180 QSGNQSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 239  
Db 182 QSGNQSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGE 241

## RESULT 3

US-08-398-613A-56  
; Sequence 56, Application US/08398613A  
; Patent No. 5677426  
; GENERAL INFORMATION:  
; APPLICANT: Fong, Sherman  
; APPLICANT: Hebert, Caroline Alice  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398,613A  
; FILING DATE: 01-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 874P1-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1489  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-398-613A-56

Query Match 78.6%; Score 976; DB 1; Length 242;  
Best Local Similarity 84.5%; Pred. No. 5.6e-78;  
Matches 185; Conservative 16; Mismatches 18; Indels 0; Gaps 0;  
QY 21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQOKPGOPRLLIYKVSND 80  
Db 24 DIVMTQSPLSLPVSLGDAQSISCRSSQSLVHGIGNYLVHLYLQKQSPKLLIYKVSND 83  
QY 81 SGVPRFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRTPTFGGKTVEIKRTVAAPSV 140  
Db 84 SGVPRFSGSGAGTDFTLKISAVEAEDVGVYFCQGTTRTPTFGGKTVEIKRTVAAPSV 143  
QY 141 FIFPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKSTYS 200  
Db 144 FIFPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKSTYS 203

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 8.49182 Seconds  
(without alignments)  
828.100 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSPLPALLGLLLCVPGSSG.....EVTHQGLSPVTKSFRNGEC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCFUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	239	3	US-08-487-550-6
2	978	78.7	241	2	US-07-916-098A-56
3	976	78.6	242	1	US-08-398-613A-56
4	976	78.6	242	1	US-08-398-612A-56
5	976	78.6	242	1	US-08-398-611A-56
6	976	78.6	242	2	US-08-491-334A-56
7	976	78.6	242	3	US-09-027-449-42
8	976	78.6	242	3	US-08-804-444A-42
9	976	78.6	242	4	US-09-026-985-42
10	976	78.6	242	4	US-09-121-952A-42
11	976	78.6	242	4	US-09-234-340A-42
12	975.5	75.5	240	4	US-09-301-593-36
13	939.5	75.6	234	4	US-09-049-672A-6
14	936	75.4	242	3	US-09-027-449-62
15	936	75.4	242	4	US-09-026-985-62
16	936	75.4	242	4	US-09-121-952A-62
17	936	75.4	242	4	US-09-234-340A-62
18	935	75.3	242	3	US-09-027-449-51
19	935	75.3	242	3	US-08-804-444A-51
20	935	75.3	242	4	US-09-026-985-51
21	935	75.3	242	4	US-09-121-952A-51
22	935	75.3	242	4	US-09-234-340A-51
23	932	75.0	219	3	US-08-027-449-72
24	932	75.0	219	4	US-09-026-985-72
25	932	75.0	219	4	US-09-121-952A-72
26	932	75.0	219	4	US-09-234-340A-72
27	932	75.0	242	3	US-09-027-449-56

28	932	75.0	242	3	US-08-804-444A-56	Sequence 56, Appl
29	932	75.0	242	4	US-09-026-985-56	Sequence 56, Appl
30	932	75.0	242	4	US-09-121-952A-56	Sequence 56, Appl
31	932	75.0	242	4	US-09-234-340A-56	Sequence 56, Appl
32	928.5	74.8	240	4	US-09-301-593-28	Sequence 28, Appl
33	909.5	73.2	220	4	US-08-952-235-1	Sequence 1, Appl
34	909.5	73.2	220	4	US-09-669-971-1	Sequence 1, Appl
35	900.5	72.5	235	3	US-08-812-586-16	Sequence 16, Appl
36	900	72.5	235	1	US-08-276-852-153	Sequence 153, App
37	900	72.5	235	1	US-08-899-575-153	Sequence 153, App
38	900	72.5	235	1	US-08-899-575-153	Sequence 153, App
39	900	72.5	235	5	PCT-US95-08743-153	Sequence 153, App
40	899.5	72.4	236	1	US-08-157-101A-5	Sequence 5, Appl
41	893.5	71.9	218	5	PCT-US96-13152-2	Sequence 2, Appl
42	893.5	71.9	220	4	US-09-301-593-17	Sequence 17, Appl
43	888.5	71.5	233	2	US-07-934-373C-25	Sequence 25, Appl
44	888.5	71.5	233	3	US-08-437-642B-25	Sequence 25, Appl
45	888.5	71.5	233	4	US-08-146-206C-25	Sequence 25, Appl

## ALIGNMENTS

## RESULT 1

US-08-487-550-6

; Sequence 6, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 6:

; LENGTH: 239 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-487-550-6

Query Match 100.0%; Score 1242; DB 3; Length 239;

Best Local Similarity 100.0%; Pred. No. 3.1e-101;

Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPLPALLGLLLCVPGSSGVVMTQSPSLPITPGSPASISCRSSQSLKHSNGDTFLSW 60

Db 1 MSPLPALLGLLLCVPGSSGVVMTQSPSLPITPGSPASISCRSSQSLKHSNGDTFLSW 60



; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/225,757  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/226,868  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/216,647  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,267  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/216,880  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,270  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/251,869  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/235,834  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/234,274  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/234,223  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/228,924  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/224,518  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,369  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/224,519  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,964  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/241,809  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/249,299  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/236,327  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/241,785  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/244,617  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 60/225,268  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,368  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/251,856  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/251,868  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/229,344  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: 60/229,343  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,345  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,287  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,513  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/231,413  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/229,509  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/236,367  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/237,039  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,038  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/236,370  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/236,802  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,037  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,040  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/239,935  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/239,937  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/241,787  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,474  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/246,532  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/249,216  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,210  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/226,681  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,759  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/225,213  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/227,182  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,214  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/235,836  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/230,438  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/215,135  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/225,266  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/249,218  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,208  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,213  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,212  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,207  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,245  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,244  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,217  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,211  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,215  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,264

```
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Nakahara, Kaori
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
; FILE REFERENCE: 980125/HG
; CURRENT APPLICATION NUMBER: US/09/046,351A
; CURRENT FILING DATE: 1998-03-23
; EARLIER APPLICATION NUMBER: JP HEI 9-67938
; EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-09-046-351-82

Query Match      89.6%; Score 1113; DB 14; Length 239;
Best Local Similarity 90.0%; Pred. No. 1.3e-86;
Matches 215; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSPLPAQLLGLLLLCVPGSSGEVVMVTQSPLSLPTTPGPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MRLPAQLLGLLLMLVPGSSGDVVMVTQSPLSLPTVTLGQPASISCRSSKSLVHSGNTYLHW 60

QY 61 YQKPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDTFLKISAVEAEDVGVPFCGQGRTP 120
Db 61 YLQKPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDTFLKISRVEAEDVGVIYCSQSTHVP 120

QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQ 180
Db 121 PAFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQ 180

QY 181 SGNQESVTEQDSKDYSLSTLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQESVTEQDSKDYSLSTLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 12
US-09-046-351-78
; Sequence 78, Application US/09046351A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Nakahara, Kaori
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
; FILE REFERENCE: 980125/HG
; CURRENT APPLICATION NUMBER: US/09/046,351A
; CURRENT FILING DATE: 1998-03-23
; EARLIER APPLICATION NUMBER: JP HEI 9-67938
; EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-09-046-351-78

Query Match      89.4%; Score 1110; DB 14; Length 239;
Best Local Similarity 89.5%; Pred. No. 2.3e-86;
Matches 214; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Nakahara, Kaori
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
; FILE REFERENCE: 980125/HG
; CURRENT APPLICATION NUMBER: US/09/046,351A
; CURRENT FILING DATE: 1998-03-23
; EARLIER APPLICATION NUMBER: JP HEI 9-67938
; EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-09-046-351-78
```

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QY 1 MSPLPAQLLGLLLLCVPGSSGEVVMVTQSPLSLPTTPGPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MRLPAQLLGLLLMLVPGSSGDVVMVTQSPLSLPTVTLGQPASISCRSSKSLVHSGNTYLHW 60

QY 61 YQKPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDTFLKISAVEAEDVGVPFCGQGRTP 120
Db 61 YLQKPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDTFLKISRVEAEDVGVIYCSQSTHVP 120

QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQ 180
Db 121 PAFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQ 180

QY 181 SGNQESVTEQDSKDYSLSTLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 239
Db 181 SGNQESVTEQDSKDYSLSTLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 13
US-09-760-479-641
; Sequence 641, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760,479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 641
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-479-641

Query Match      87.8%; Score 1091; DB 21; Length 244;
Best Local Similarity 87.4%; Pred. No. 9.9e-85;
Matches 209; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSPLPAQLLGLLLLCVPGSSGEVVMVTQSPLSLPTTPGPASISCRSSQSLKHSNGDTFLSW 60
Db 6 MRLPAQLLGLLLMLVPGSSGDIWMTQTPLSSPVTLQGPASISCRSNQSLVHSDGNTYLSW 65

QY 61 YQKPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDTFLKISAVEAEDVGVPFCGQGRTP 120
Db 66 LQORPGQPPRLLIYKVNRSRGVDPDRFSGSGAGTDTFLKITRVEAEDVGVIYCMQATQFP 125

QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQ 180
Db 126 LTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQ 185

QY 181 SGNQESVTEQDSKDYSLSTLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 239
Db 186 SGNQESVTEQDSKDYSLSTLTLSKADYKHKYKIVACEVTHQGLSSPVTKSFNRGEC 244

RESULT 14
US-10-206-008-641
; Sequence 641, Application US/10206008
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253CIN
; CURRENT APPLICATION NUMBER: US/10/206,008
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/760,479
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
```

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/124,905  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/383,916  
 FILING DATE:  
 APPLICATION NUMBER: US 08/487,550  
 FILING DATE: 07-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Teskin, Robin L.  
 REGISTRATION NUMBER: 35,030  
 REFERENCE/DOCKET NUMBER: 012712-131  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620  
 TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 239 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-10-124-905-6

Query Match 100.0%; Score 1242; DB 25; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-97;  
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 DB 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 QY 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGDTFTLKISAVEAEDVGVYFCQGRTTP 120  
 DB 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGDTFTLKISAVEAEDVGVYFCQGRTTP 120  
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
 DB 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
 QY 181 SGNSESVEQDSKDSSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
 DB 181 SGNSESVEQDSKDSSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 9  
 US-09-046-351-84  
 ; Sequence 84, Application US/09046351A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Serizawa, Nobufusa  
 ; APPLICANT: Haruyama, Hideyuki  
 ; APPLICANT: Takahashi, Tohru  
 ; APPLICANT: Nakahara, Kaori  
 ; APPLICANT: Yonehara, Shin  
 ; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY  
 ; FILE REFERENCE: 980125/HG  
 ; CURRENT APPLICATION NUMBER: US/09/046,351A  
 ; EARLIER FILING DATE: 1998-03-23  
 ; EARLIER FILING DATE: 1997-03-21  
 ; NUMBER OF SEQ ID NOS: 189  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 84  
 ; LENGTH: 239  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: L chain of a  
 ; OTHER INFORMATION: humanized anti-Fas antibody

US-09-046-351-84  
 Query Match 89.9%; Score 1116; DB 14; Length 239;  
 Best Local Similarity 90.4%; Pred. No. 6.9e-87;  
 Matches 216; Conservative 8; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 DB 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 QY 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGDTFTLKISAVEAEDVGVYFCQGRTTP 120  
 DB 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGDTFTLKISAVEAEDVGVYFCQGRTTP 120  
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
 DB 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
 QY 181 SGNSESVEQDSKDSSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
 DB 181 SGNSESVEQDSKDSSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
 RESULT 10  
 US-09-046-351-80  
 ; Sequence 80, Application US/09046351A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Serizawa, Nobufusa  
 ; APPLICANT: Haruyama, Hideyuki  
 ; APPLICANT: Takahashi, Tohru  
 ; APPLICANT: Nakahara, Kaori  
 ; APPLICANT: Yonehara, Shin  
 ; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY  
 ; FILE REFERENCE: 980125/HG  
 ; CURRENT APPLICATION NUMBER: US/09/046,351A  
 ; EARLIER FILING DATE: 1998-03-23  
 ; EARLIER FILING DATE: 1997-03-21  
 ; NUMBER OF SEQ ID NOS: 189  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 80  
 ; LENGTH: 239  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: L chain of a  
 ; OTHER INFORMATION: humanized anti-Fas antibody  
 US-09-046-351-80

Query Match 89.6%; Score 1113; DB 14; Length 239;  
 Best Local Similarity 90.0%; Pred. No. 1.3e-86;  
 Matches 215; Conservative 9; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 DB 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 QY 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGDTFTLKISAVEAEDVGVYFCQGRTTP 120  
 DB 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGDTFTLKISAVEAEDVGVYFCQGRTTP 120  
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
 DB 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
 QY 181 SGNSESVEQDSKDSSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
 DB 181 SGNSESVEQDSKDSSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
 RESULT 11  
 US-09-046-351-82  
 ; Sequence 82, Application US/09046351A



;; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
;; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
;; STREET: 699 Prince Street  
;; CITY: Alexandria  
;; STATE: VA  
;; COUNTRY: USA  
;; ZIP: 22314

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/030,390  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/383,916  
;; FILING DATE:  
;; APPLICATION NUMBER: US 08/487,550  
;; FILING DATE: 07-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Teskin, Robin L.  
;; REGISTRATION NUMBER: 35,030  
;; REFERENCE/DOCKET NUMBER: 012712-131  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-836-6620  
;; TELEFAX: 703-836-6620  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 239 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-10-030-390-6

Query Match 100.0%; Score 1242; DB 24; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.1e-97;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPLAQLGLLLCVPGSGEVVMTQSPLSLPTTGPASISCRSSQSLKHSNGDTFLSW 60  
DB 1 MSPLAQLGLLLCVPGSGEVVMTQSPLSLPTTGPASISCRSSQSLKHSNGDTFLSW 60  
QY 61 YQKPGQPPRLLIYKVSNRDGVDPDRFSGSGAGTDTLTKISAVEAEDVGVYFCGGGTRTP 120  
DB 61 YQKPGQPPRLLIYKVSNRDGVDPDRFSGSGAGTDTLTKISAVEAEDVGVYFCGGGTRTP 120  
QY 121 PTFGGKTVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ 180  
DB 121 PTFGGKTVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ 180  
QY 181 SGNQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SGNQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 7  
US-10-124-807-6  
; Sequence 6, Application US/10124807  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

;; STREET: 699 Prince Street  
;; CITY: Alexandria  
;; STATE: VA  
;; COUNTRY: USA  
;; ZIP: 22314  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/124,807  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/383,916  
;; FILING DATE:  
;; APPLICATION NUMBER: US 08/487,550  
;; FILING DATE: 07-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Teskin, Robin L.  
;; REGISTRATION NUMBER: 35,030  
;; REFERENCE/DOCKET NUMBER: 012712-131  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-836-6620  
;; TELEFAX: 703-836-2021  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 239 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-10-124-807-6

Query Match 100.0%; Score 1242; DB 25; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.1e-97;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPLAQLGLLLCVPGSGEVVMTQSPLSLPTTGPASISCRSSQSLKHSNGDTFLSW 60  
DB 1 MSPLAQLGLLLCVPGSGEVVMTQSPLSLPTTGPASISCRSSQSLKHSNGDTFLSW 60  
QY 61 YQKPGQPPRLLIYKVSNRDGVDPDRFSGSGAGTDTLTKISAVEAEDVGVYFCGGGTRTP 120  
DB 61 YQKPGQPPRLLIYKVSNRDGVDPDRFSGSGAGTDTLTKISAVEAEDVGVYFCGGGTRTP 120  
QY 121 PTFGGKTVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ 180  
DB 121 PTFGGKTVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ 180  
QY 181 SGNQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SGNQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8  
US-10-124-905-6  
; Sequence 6, Application US/10124905  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
Db 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 4  
US-09-758-173-6  
; Sequence 6, Application US/09758173  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/758,173  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/383,916  
; FILING DATE:  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-758-173-6

Query Match 100.0%; Score 1242; DB 21; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.le-97;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLLCVPGSSGEVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
Db 1 MSLPAQLGLLLLCVPGSSGEVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60

QY 61 YQKPGQPPRLLIYKVNRSNDRSGVDFRSGSGAGDTFTLKISAVEAEDVGIVFCQGTRTP 120  
Db 61 YQKPGQPPRLLIYKVNRSNDRSGVDFRSGSGAGDTFTLKISAVEAEDVGIVFCQGTRTP 120

QY 121 PTFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
Db 121 PTFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
Db 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 5  
US-09-948-429B-6  
; Sequence 6, Application US/09948429B  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/948,429B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/383,916  
; FILING DATE:  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-948-429B-6

Query Match 100.0%; Score 1242; DB 23; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.le-97;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLLCVPGSSGEVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
Db 1 MSLPAQLGLLLLCVPGSSGEVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60

QY 61 YQKPGQPPRLLIYKVNRSNDRSGVDFRSGSGAGDTFTLKISAVEAEDVGIVFCQGTRTP 120  
Db 61 YQKPGQPPRLLIYKVNRSNDRSGVDFRSGSGAGDTFTLKISAVEAEDVGIVFCQGTRTP 120

QY 121 PTFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
Db 121 PTFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180

QY 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
Db 181 SGNQSVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 6  
US-10-030-390-6  
; Sequence 6, Application US/10030390  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-383-916-6

Query Match 100.0%; Score 1242; DB 17; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.1e-97;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60  
DB 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60  
QY 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCGQGTTRTP 120  
DB 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCGQGTTRTP 120  
QY 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQ 180  
DB 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQ 180  
QY 181 SGNSESVEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SGNSESVEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 2

US-09-526-098-6  
Sequence 6, Application US/09526098  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/526,098  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-526-098-6

Query Match 100.0%; Score 1242; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.1e-97;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60  
DB 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60  
QY 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCGQGTTRTP 120  
DB 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCGQGTTRTP 120  
QY 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQ 180  
DB 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQ 180  
QY 181 SGNSESVEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SGNSESVEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 3

US-09-576-424-6  
Sequence 6, Application US/09576424  
GENERAL INFORMATION:  
APPLICANT: ANDERSON, DARRELL R.  
APPLICANT: HANNA, NABIL  
APPLICANT: BRAMS, PETER  
APPLICANT: HEARD, CHERYL  
TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2  
TITLE OF INVENTION: CO-STIMULATORY ANTIGENS  
FILE REFERENCE: 37003-275681  
CURRENT APPLICATION NUMBER: US/09/576,424  
CURRENT FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: PCT/US97/19906  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 08/746,361  
PRIOR FILING DATE: 1996-11-08  
PRIOR APPLICATION NUMBER: 08/487,550  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 6  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-576-424-6

Query Match 100.0%; Score 1242; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.1e-97;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60  
DB 1 MSLPAQLGLLLLCVPGSSGEVVMVTQSPSLPTTPGEPASISCRSSQSLKHSNGDTFLSW 60  
QY 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCGQGTTRTP 120  
DB 61 YQKPGQPPRLIIYKVNRSQVDPDRFSGSGAGTDTFLKISAVEAEDVGVYFCGQGTTRTP 120  
QY 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQ 180  
DB 121 PTFGGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQ 180

GenCore version 5.1.4.p5 4578  
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:10:32 ; Search time 109.835 Seconds  
(without alignments)  
1402.934 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242  
Sequence: 1 MSLPQALLGLLLCVPOSSG.....EVTHQGLSSPTKSNRGECC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:\*

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3: /cgn2\_6/ptodata/1/paa/US07 COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*  
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8: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*  
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24: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*  
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26: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*  
27: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	239	17	US-09-383-916-6
2	1242	100.0	239	19	US-09-526-098-6
3	1242	100.0	239	19	US-09-576-424-6
4	1242	100.0	239	21	US-09-758-173-6
5	1242	100.0	239	23	US-09-948-429B-6
6	1242	100.0	239	24	US-10-030-390-6

7	1242	100.0	239	25	US-10-124-807-6
8	1242	100.0	239	25	US-10-124-807-6
9	1113	89.6	239	14	US-09-046-351-84
10	1113	89.6	239	14	US-09-046-351-80
11	1113	89.6	239	14	US-09-046-351-82
12	1110	89.4	239	14	US-09-046-351-78
13	1091	87.8	244	21	US-09-760-479-641
14	1091	87.8	244	26	US-10-206-008-641
15	1073	86.4	262	21	US-09-760-479-658
16	1073	86.4	262	26	US-10-206-008-658
17	1070.5	86.2	238	1	PCT-US02-11854A-19
18	1069	86.1	239	25	US-10-108-260A-4028
19	1068	86.0	239	23	US-09-924-340-8
20	1068	86.0	239	23	US-09-992-600A-8
21	1068	86.0	239	23	US-09-994-590-8
22	1068	86.0	239	24	US-10-000-489-8
23	1068	86.0	239	24	US-10-000-986-8
24	1068	86.0	239	27	US-60-305-456-8
25	1052.5	84.7	238	11	US-08-721-612B-19
26	1052.5	84.7	238	11	US-08-721-612C-19
27	1052.5	84.7	238	11	US-08-721-612D-19
28	1052.5	84.7	238	11	US-08-721-612E-19
29	1042	83.9	241	22	US-09-831-805A-15
30	1042	83.9	241	27	US-60-128-194-1
31	1041	83.8	239	1	PCT-US02-11853-19
32	1033	83.2	219	1	PCT-US02-11854A-11
33	1014	81.6	217	21	US-09-791-537-116780
34	1011	81.4	217	21	US-09-791-537-116791
35	1009	81.2	219	1	PCT-US02-21323-11
36	1009	81.2	219	1	PCT-US02-21324-11
37	1009	81.2	219	1	PCT-US02-26321-11
38	1008	81.2	219	23	US-09-972-656-92
39	1007	81.1	238	24	US-10-031-355-2
40	1007	81.1	238	24	US-10-031-355-11
41	1007	81.1	238	24	US-10-031-355-13
42	1007	81.1	238	24	US-10-031-355-15
43	1004	80.8	219	1	PCT-US02-11853-11
44	997	80.3	219	23	US-09-972-656-106
45	992.5	79.9	220	22	US-09-822-698A-24

## ALIGNMENTS

### RESULT 1

US-09-383-916-6

; Sequence 6, Application US/09383916

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/09/383,916

; FILING DATE: 26-AUG-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA: US 08/487,550

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995



INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-726-258-72

Query Match 75.0%; Score 932; DB 9; Length 219;  
Best Local Similarity 81.7%; Pred. No. 6.1e-40;  
Matches 179; Conservative 14; Mismatches 26; Indels 0; Gaps 0;  
QY 21 EYVMTQSPSLSPITPGEPASISCRSSQSLKHSNGDTFLSWYQKQKPGQPPRLIIYKVNRD 80  
DB 1 DIQMTQSPSSLSASVGRVTITCRSSQSLVHGIGATYHLHWYQKQKAPKLLIYKVNRF 60  
QY 81 SGVPRFSGSGAGTDFTLKISAVEAEADVGYFCGQGTPTPTFGGTTKVEIKRTVAAPSV 140  
DB 61 SGVPRFSGSGAGTDFTLTISLQPEDFATYYCSQSTHVPLTFGQGTVEIKRTVAAPSV 120  
QY 141 FIFPDSQQLSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200  
DB 121 FIFPDSQQLSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180  
QY 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 15  
US-09-726-258-56  
Sequence 56, Application US/09726258  
Publication No. US20030021790A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc., Heei, Vanessa  
APPLICANT: Koumenis, Iphigenia  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Shahrokh, Zahra  
APPLICANT: Zapata, Gerardo A.  
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/726,258  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/234,182  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/094003  
FILING DATE: 24-JUL-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085R4-1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/252-9881  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:

LENGTH: 242 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-726-258-56

Query Match 75.0%; Score 932; DB 9; Length 242;  
Best Local Similarity 81.7%; Pred. No. 6.6e-40;  
Matches 179; Conservative 14; Mismatches 26; Indels 0; Gaps 0;  
QY 21 EYVMTQSPSLSPITPGEPASISCRSSQSLKHSNGDTFLSWYQKQKPGQPPRLIIYKVNRD 80  
DB 24 DIQMTQSPSSLSASVGRVTITCRSSQSLVHGIGATYHLHWYQKQKAPKLLIYKVNRF 83  
QY 81 SGVPRFSGSGAGTDFTLKISAVEAEADVGYFCGQGTPTPTFGGTTKVEIKRTVAAPSV 140  
DB 84 SGVPRFSGSGAGTDFTLTISLQPEDFATYYCSQSTHVPLTFGQGTVEIKRTVAAPSV 143  
QY 141 FIFPDSQQLSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200  
DB 144 FIFPDSQQLSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 203  
QY 201 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
DB 204 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 242

Search completed: March 29, 2003, 09:38:39  
Job time: 11.1622 secs

; REFERENCE/DOCKET NUMBER: P1085R4-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-726-258-62

Query Match 75.4%; Score 936; DB 9; Length 242;  
Best Local Similarity 81.7%; Pred. No. 4.2e-40;  
Matches 179; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

Qy 21 EVWVTQSPSLPIPTGEPASISCRSSQSLKHSNGDTFLSWYQKQKPGQPPRLIIYKVSNRD 80  
Db 24 DIQWTSPPSSLSASVGRVITICRSSQSLVHGIGETYLHWYQKPGKAPKLLIYKVSNR 83  
Qy 81 SGVPDRFSGSGAGTDFTLTKISAVEAEDVGVFYFCGQGTPTPTFGGQTKVEIKRTVAAPSV 140  
Db 84 SGVPSRFSGSGGTDFLTITISSLPQDPFATYYCSQSTHVPLTFGQGTKEIKRTVAAPSV 143  
Qy 141 FIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 200  
Db 144 FIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 203  
Qy 201 SSTLTLSKADYKHKYVACEVTHOGLSSPVTKSFNRGEC 239  
Db 204 SSTLTLSKADYKHKYVACEVTHOGLSSPVTKSFNRGEC 242

RESULT 13  
US-09-726-258-51

; Sequence 51, Application US/09726258  
; Publication No. US20030021790A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Hsai, Vanessa  
; APPLICANT: Koumenis, Iphigenia  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Shahrokhi, Zahra  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND  
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/726,258  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/234,182  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/094003  
; FILING DATE: 24-JUL-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R4-1A  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-726-258-51

Query Match 75.3%; Score 935; DB 9; Length 242;  
Best Local Similarity 81.7%; Pred. No. 4.7e-40;  
Matches 179; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

Qy 21 EVWVTQSPSLPIPTGEPASISCRSSQSLKHSNGDTFLSWYQKQKPGQPPRLIIYKVSNRD 80  
Db 24 DIQWTSPPSSLSASVGRVITICRSSQSLVHGIGETYLHWYQKPGKAPKLLIYKVSNR 83  
Qy 81 SGVPDRFSGSGAGTDFTLTKISAVEAEDVGVFYFCGQGTPTPTFGGQTKVEIKRTVAAPSV 140  
Db 84 SGVPSRFSGSGGTDFLTITISSLPQDPFATYYCSQSTHVPLTFGQGTKEIKRTVAAPSV 143  
Qy 141 FIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 200  
Db 144 FIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQBSVTEQDSKDYSL 203  
Qy 201 SSTLTLSKADYKHKYVACEVTHOGLSSPVTKSFNRGEC 239  
Db 204 SSTLTLSKADYKHKYVACEVTHOGLSSPVTKSFNRGEC 242

RESULT 14

US-09-726-258-72  
; Sequence 72, Application US/09726258  
; Publication No. US20030021790A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Hsai, Vanessa  
; APPLICANT: Koumenis, Iphigenia  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Shahrokhi, Zahra  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND  
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/726,258  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/234,182  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/094003  
; FILING DATE: 24-JUL-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R4-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881

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QY 60 WYQKPGQPPRLIIYKVNDRSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGGTGT 119
Db 61 WYQKPGQPPKLLIYASTRESGVDPDRFSGSGGTDFTLTISSLAEDVAVYVYCCQYYST 120
QY 120 PPTFGGKTVEIKRTVAAPSVFIIPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNAL 179
Db 121 PYSGGQGTKEIKRTVAAPSVFIIPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNAL 180
QY 180 QSGNSQESVTEQDSKDYSLSTLTLKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239
Db 181 QSGNSQESVTEQDSKDYSLSTLTLKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 240
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RESULT 10
US-09-859-053-34
; Sequence 34, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34
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Query Match 76.1%; Score 945.5; DB 10; Length 236;
Best Local Similarity 77.1%; Pred. No. 1.4e-40;
Matches 185; Conservative 25; Mismatches 25; Indels 5; Gaps 2;

QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTPSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 METPAQLFLLLWLPTTGEIVLTQSPGTLSPGERATLSCRAQNISS----YLAW 56

QY 61 YQKPGQPPRLIIYKVNDRSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQ-GTGT 119
Db 57 YQKPGQAPGLLIYAGSSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYVYCCQFGSSP 116

QY 120 PPTFGGKTVEIKRTVAAPSVFIIPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNAL 179
Db 117 MCSFGQGTKEIKRTVAAPSVFIIPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNAL 176

QY 180 QSGNSQESVTEQDSKDYSLSTLTLKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239
Db 177 QSGNSQESVTEQDSKDYSLSTLTLKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 236
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RESULT 11
US-09-859-053-38
; Sequence 38, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
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; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-38
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Query Match 75.7%; Score 940.5; DB 10; Length 236;
Best Local Similarity 77.1%; Pred. No. 2.5e-40;
Matches 185; Conservative 24; Mismatches 26; Indels 5; Gaps 2;

QY 1 MSLPAQLGLLLLCVPGSSGEVVMVTPSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 METPAQLFLLLWLPTTGEIVLTQSPGTLSPGERATLSCRAQNISS----LAW 56

QY 61 YQKPGQPPRLIIYKVNDRSGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQ-GTGT 119
Db 57 YQKPGQAPGLLIYAGSSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYVYCCQFGSSP 116

QY 120 PPTFGGKTVEIKRTVAAPSVFIIPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNAL 179
Db 117 MCSFGQGTKEIKRTVAAPSVFIIPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNAL 176

QY 180 QSGNSQESVTEQDSKDYSLSTLTLKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 239
Db 177 QSGNSQESVTEQDSKDYSLSTLTLKADYKHKYKVAACEVTHQGLSSPVTKSFNRGEC 236
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RESULT 12
US-09-726-258-62
; Sequence 62, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsai, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/234,182
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/094003
; FILING DATE: 24-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
```





US-09-992-600A-8  
; Sequence 8, Application US/09992600A  
; Publication No. US20030027161A1  
; GENERAL INFORMATION:  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Benjanin, Stephanie  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.054.DIV  
; CURRENT APPLICATION NUMBER: US/09/992,600A  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: JPatent  
; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
US-09-992-600A-8  
Query Match 86.0%; Score 1068; DB 9; Length 239;  
Best Local Similarity 86.6%; Pred. No. 1.2e-46;  
Matches 207; Conservative 11; Mismatches 21; Indels 0; Gaps 0;  
QY 1 MSLLPAQLGILLVCVPGSGSEVMTQSPISLPTTPGEPASISCRSSQSLKHNGSDTFLSW 60  
DB 1 MRLPAQLGILLMLVWSSGSDIVMTQSPILFPTVTPGEPASISCRSSQSLHVVQGSNYLDW 60  
QY 61 YQKPGQPRLLYKYVNRDSDVDPDRFSGSGAGTDTFLKISAVEADVGVYFCGGCTRTTP 120  
DB 61 YHQPQSPOLLILYLGNSRAGVDPDRFSGSGGTDTFLKISVEADVGVYCYCQALQTP 120  
QY 121 PTFGGGTKEIKRTVAAPSFIIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQ 180  
DB 121 FTGPGTRVDIKETVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQ 180  
QY 181 SGNQSQSVTEQDSKDYSLSSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SGNQSQSVTEQDSKDYSLSSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239  
RESULT 5  
US-09-822-698A-24  
; Sequence 24, Application US/09822698A  
; Patent No. US20020146750A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Maria P.G.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DYX-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 24  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: artificial sequence

; FEATURE:  
; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1  
US-09-822-698A-24  
Query Match 79.9%; Score 992.5; DB 10; Length 220;  
Best Local Similarity 87.7%; Pred. No. 6.3e-43;  
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
QY 21 EVNMTQSPISLPTTPGEPASISCRSSQSLKHNGSDTFLSWYQKPGQPRLLYKYVNRD 80  
DB 1 EIVLTQSPISLPTTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLYYSGSHRA 60  
QY 81 SGVDPDRFSGSGAGTDTFLKISAVEADVGVYFCGGCTRTTPTEGGGTKEIKR-TVAAPS 139  
DB 61 SGVDPDRFSGSVSGTDTFLRISVEADVGVYCYCQGLSPFTFGPGTKVDIKKGTVAAPS 120  
QY 140 VFIPPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKDYSL 199  
DB 121 VFIPPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKDYSL 180  
QY 200 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220  
RESULT 6  
US-09-726-258-42  
; Sequence 42, Application US/09726258  
; Publication No. US20030021790A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc., Hsei, Vanessa  
; APPLICANT: Koumenis, Iphigenia  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Zapata, Gerardo A.  
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND  
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/726,258  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/234,182  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/094003  
; FILING DATE: 24-JUL-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R4-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-10-124-905-6

Query Match 100.0%; Score 1242; DB 9; Length 239;  
Best Local Similarity 100.0%; Pred. No. 3.1e-55;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSGGVVMTQSPSLPTTGPSPASISCRSSQSLKHSNGDTFLSW 60  
DB 1 MSLPAQLGLLLCVPGSGGVVMTQSPSLPTTGPSPASISCRSSQSLKHSNGDTFLSW 60

QY 61 YQKPGQPPRLLIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTTP 120  
DB 61 YQKPGQPPRLLIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTTP 120

QY 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180  
DB 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180

QY 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 2  
US-09-948-429B-6  
Sequence 6, Application US/09948429B  
Patent No. US2002017769A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESS: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/948,429B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teekin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-948-429B-6

Query Match 100.0%; Score 1242; DB 9; Length 239;  
Best Local Similarity 100.0%; Pred. No. 3.1e-55;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSGGVVMTQSPSLPTTGPSPASISCRSSQSLKHSNGDTFLSW 60  
DB 1 MSLPAQLGLLLCVPGSGGVVMTQSPSLPTTGPSPASISCRSSQSLKHSNGDTFLSW 60

QY 61 YQKPGQPPRLLIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTTP 120  
DB 61 YQKPGQPPRLLIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTTP 120

QY 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180  
DB 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180

QY 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 3  
US-09-924-340-8  
Sequence 8, Application US/09924340  
Publication No. US20030027248A1  
GENERAL INFORMATION:  
APPLICANT: Bejanin, Stephane  
APPLICANT: Tanaka, Hiroaki  
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
FILE REFERENCE: 91 US2 REG  
CURRENT APPLICATION NUMBER: US/09/924,340  
PRIOR FILING DATE: 2001-08-06  
PRIOR APPLICATION NUMBER: US 60/305,456  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: US 60/302,277  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/298,698  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: US 60/293,574  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: JPatent  
SEQ ID NO 8  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: 1..20  
US-09-924-340-8

Query Match 86.0%; Score 1068; DB 9; Length 239;  
Best Local Similarity 86.6%; Pred. No. 1.2e-46;  
Matches 207; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSGGVVMTQSPSLPTTGPSPASISCRSSQSLKHSNGDTFLSW 60  
DB 1 MSLPAQLGLLLCVPGSGGVVMTQSPSLPTTGPSPASISCRSSQSLKHSNGDTFLSW 60

QY 61 YQKPGQPPRLLIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTTP 120  
DB 61 YQKPGQPPRLLIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTTP 120

QY 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180  
DB 121 PTFGGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180

QY 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239  
DB 181 SGNQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 4

GenCore version 5.1.4 p5 4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2003, 09:14:52 ; Search time 9.16222 Seconds  
(without alignments)  
1531.829 Million cell updates/sec

Title: US-09-758-173-6  
Perfect score: 1242  
Sequence: 1 MSIPALQLGLLLCVPGSSG.....EVTHQGLSPVTKSNRQEC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

Published Applications AA:  
1: /cgn2\_6/ptodata/1/pubaa/US08\_NEW\_PUB.pdb.\*  
2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pdb.\*  
3: /cgn2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pdb.\*  
4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pdb.\*  
5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pdb.\*  
6: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pdb.\*  
7: /cgn2\_6/ptodata/1/pubaa/PCTUS\_PUBCOMB.pdb.\*  
8: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pdb.\*  
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11: /cgn2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pdb.\*  
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14: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	239	9 US-10-124-905-6	Sequence 6, Appli
2	1242	100.0	239	9 US-09-948-429B-6	Sequence 6, Appli
3	1068	86.0	239	9 US-09-924-340-8	Sequence 8, Appli
4	1068	86.0	239	9 US-09-992-600A-8	Sequence 8, Appli
5	992.5	79.9	220	10 US-09-822-698A-24	Sequence 24, Appl
6	976	78.6	242	9 US-09-726-258-42	Sequence 42, Appl
7	960.5	77.3	228	9 US-09-909-567B-50	Sequence 50, Appl
8	960	77.3	239	9 US-09-249-011A-22	Sequence 22, Appl
9	954.5	76.9	240	10 US-09-799-514-8	Sequence 8, Appli
10	945.5	76.1	236	10 US-09-859-053-34	Sequence 34, Appl
11	940.5	75.7	236	10 US-09-859-053-38	Sequence 38, Appl
12	936	75.4	242	9 US-09-726-258-62	Sequence 62, Appl
13	935	75.3	242	9 US-09-726-258-51	Sequence 51, Appl
14	932	75.0	219	9 US-09-726-258-72	Sequence 72, Appl
15	932	75.0	242	9 US-09-726-258-56	Sequence 56, Appl
16	924.5	74.4	236	10 US-09-859-053-30	Sequence 30, Appl
17	909.5	73.2	220	10 US-09-955-693-1	Sequence 1, Appli
18	904.5	72.8	234	10 US-09-740-002-24	Sequence 24, Appl
19	901.5	72.6	236	9 US-10-006-593-69	Sequence 69, Appl

20	898.5	72.3	239	10 US-09-825-012-9	Sequence 9, Appli
21	893.5	71.9	218	10 US-09-917-410-2	Sequence 2, Appli
22	892.5	71.9	218	9 US-09-925-179-67	Sequence 67, Appli
23	892.5	71.9	220	10 US-09-917-410-5	Sequence 5, Appli
24	887	71.4	242	9 US-09-479-614-20	Sequence 20, Appli
25	885.5	71.3	218	9 US-09-925-179-9	Sequence 9, Appli
26	885.5	71.3	218	10 US-09-802-077-9	Sequence 9, Appli
27	885.5	71.3	218	10 US-09-802-096-9	Sequence 9, Appli
28	885.5	71.3	218	10 US-09-920-171-13	Sequence 13, Appli
29	883.5	71.1	214	10 US-09-940-166A-2	Sequence 2, Appli
30	883.5	71.1	214	10 US-09-811-384-11	Sequence 11, Appli
31	883.5	71.1	237	10 US-09-940-166A-6	Sequence 6, Appli
32	880.5	70.9	234	10 US-09-800-729-150	Sequence 150, Appl
33	880	70.9	235	10 US-09-910-059-97	Sequence 97, Appl
34	879	70.8	235	10 US-09-800-729-152	Sequence 152, Appl
35	877	70.6	235	10 US-09-910-059-52	Sequence 52, Appli
36	876.5	70.6	212	12 US-10-011-135-5	Sequence 15, Appli
37	875.5	70.5	218	10 US-09-920-171-15	Sequence 15, Appli
38	875.5	70.5	218	10 US-09-920-171-17	Sequence 17, Appli
39	875.5	70.5	218	10 US-09-920-171-19	Sequence 19, Appli
40	875.5	70.5	218	10 US-09-920-171-24	Sequence 24, Appli
41	875	70.5	234	10 US-09-740-002-26	Sequence 26, Appli
42	874.5	70.4	212	9 US-10-006-593-118	Sequence 118, Appl
43	871	70.1	235	10 US-09-910-059-99	Sequence 99, Appli
44	865	69.6	235	10 US-09-910-059-17	Sequence 17, Appli
45	857	69.0	669	9 US-09-807-721-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-10-124-905-6  
; Sequence 6, Application US/10124905  
; Patent No. US20020166136A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM: Floppy disk  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/124,905  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/383,916  
; FILING DATE:  
; APPLICATION NUMBER: US 08/487,550  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids



PT including metastasis, and pain

XX Claim 31; Page 34-35; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment  
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a  
 CC human PTHrP monoclonal antibody clone protein sequence from the  
 CC present invention.

XX Sequence 239 AA;

Query Match 85.7%; Score 1065; DB 21; Length 239;

Best Local Similarity 85.8%; Pred. No. 1.5e-58;

Matches 205; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSGEVMTQSPSLPITPCGPASISCRSSQSLKHNGDTFLSW 60

DB 1 MRLPAQLGLLMLVWSSGSDIVMTQSPSLPVTGPATISCRSSQSLHNRGNLYDW 60

QY 61 YQKPGQPPRLIIYKVNRSRSGVDPDRFSGSGAGTDTFLKISAVEAEDGVYFCGGQTRTP 120

DB 61 FLQKPGSQPLLIIYLGNSRASGVDPDRFSGSGGTDFTLKSRLVEAEDGLYYCMQALQIP 120

QY 121 PTFGGGTKEIKRTVAAPSVFIFPPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQ 180

DB 121 FTFGPGTKVDIKRTVAAPSVFIFPPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQ 180

QY 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

DB 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 14

AA82610

ID AAY82610 standard; Protein; 239 AA.

XX AC AAY82610;

XX 02-AUG-2000 (first entry)

XX Human PTHrP monoclonal antibody clone 15H7-8-3 protein SEQ ID NO:4.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys

FT Misc-difference 156 /label= Phe, Ser, Tyr, Cys

FT Misc-difference 164 /label= Phe, Ser, Tyr, Cys

FT /label= Phe, Leu

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-0304793.

XX

PR 17-JUN-1998; 98JP-0188196.

PR 26-JUN-1998; 98JP-0196729.

XX (NISB ) JAPAN TOBACCO INC.

XX WPI: 2000-286723/25.

XX N-PSDB; AAA13920.

PT A human monoclonal antibody to parathyroid hormone related protein. -  
 CC useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 CC including metastasis, and pain

XX Claim 31; Page 33; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment  
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a  
 CC human PTHrP monoclonal antibody clone protein sequence from the  
 CC present invention.

XX Sequence 239 AA;

Query Match 85.8%; Score 1063; DB 21; Length 239;

Best Local Similarity 86.2%; Pred. No. 1.9e-58;

Matches 206; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSGEVMTQSPSLPITPCGPASISCRSSQSLKHNGDTFLSW 60

DB 1 MRLPAQLGLLMLVWSSGSDIVMTQSPSLPVTGPATISCRSSQSLHNRGNLYDW 60

QY 61 YQKPGQPPRLIIYKVNRSRSGVDPDRFSGSGAGTDTFLKISAVEAEDGVYFCGGQTRTP 120

DB 61 YLQKPGSQPLLIIYLGNSRASGVDPDRFSGSGGTDFTLKSRLVEAEDGVYCMQALQTP 120

QY 121 PTFGGGTKEIKRTVAAPSVFIFPPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQ 180

DB 121 FTFGPGTKVDIKRTVAAPSVFIFPPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQ 180

QY 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

DB 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 15

AA82617

ID AAY82617 standard; Protein; 239 AA.

XX AC AAY82617;

XX 02-AUG-2000 (first entry)

XX Human PTHrP monoclonal antibody clone 3G4-3 protein SEQ ID NO:18.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 3 /label= Phe, Leu, Ile, Val

FT Misc-difference 4

CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
 CC chains used in the invention are represented by sequences  
 CC AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AAA78277-A78318 and  
 CC AAA78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are  
 CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer  
 CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in  
 CC the production of the agent of the invention.

XX SQ Sequence 239 AA;

Query Match 89.4%; Score 1110; DB 21; Length 239;  
 Best Local Similarity 89.5%; Pred. No. 2.4e-61;  
 Matches 214; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLLCVPSGSEVMTQSPSLPTTPGPASISCRSSQSLKHSNGDTFLSW 60  
 DB 1 MRLPAQLGLLLMLVPGSGDVMTQSPSLPTVLGQPASISCRSSKSLVHSGNTYLHW 60  
 QY 61 YQKPGOPPRLLIYKVNRSRGVDPDRFSGSGAGTDFTLKISAVEAEDGVYFCGGGTRTP 120  
 DB 61 YLQKPGQSPKLLIYKVNRSRGVDPDRFSGSGGTDFTLKISRVEAEDGVYFCSGSTHVP 120  
 QY 121 PTFGGGTKEIKRTVAAPSFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQ 180  
 DB 121 PAFGGGTKEIKRTVAAPSFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQ 180  
 QY 181 SGNSQSVTEQDSKDYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239  
 DB 181 SGNSQSVTEQDSKDYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

# RESULT 12

AA82615  
 ID AA82615 standard; Protein; 239 AA.

XX AC AA82615;

XX DT 02-AUG-2000 (first entry)

XX DE Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.

XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Misc-difference 155 /note= "possible Ala"

XX PN JP2000080100-A.

XX PD 21-MAR-2000.

XX PF 12-OCT-1998; 98JP-0304793.

XX PR 17-JUN-1998; 98JP-0188196.

XX PR 26-JUN-1998; 98JP-0196729.

XX PA (NISB ) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

XX DR N-PSDB; AAA13925.

XX PT A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain

PS Claim 31; Page 45-46; 88pp; Japanese.  
 XX CC The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment  
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a  
 CC human PTHrP monoclonal antibody clone protein sequence from the  
 CC present invention.

XX SQ Sequence 239 AA;

Query Match 87.2%; Score 1083; DB 21; Length 239;  
 Best Local Similarity 87.4%; Pred. No. 1.1e-59;  
 Matches 209; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLLCVPSGSEVMTQSPSLPTTPGPASISCRSSQSLKHSNGDTFLSW 60

DB 1 MRLPAQLGLLLMLVPGSGDVMTQSPSLPTTPGPASISCRSSQSLHSGNNYLDW 60

QY 61 YQKPGOPPRLLIYKVNRSRGVDPDRFSGSGAGTDFTLKISAVEAEDGVYFCGGGTRTP 120

DB 61 YLQKPGQSPKLLIYKVNRSRGVDPDRFSGSGGTDFTLKISRVEAEDGVYFCMAQLQTP 120

QY 121 PTFGGGTKEIKRTVAAPSFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQ 180

DB 121 PTFGGGTKEIKRTVAAPSFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQ 180

QY 181 SGNSQSVTEQDSKDYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

DB 181 SGNSQSVTEQDSKDYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239

# RESULT 13

AA82611  
 ID AA82611 standard; Protein; 239 AA.

XX AC AA82611;

XX DT 02-AUG-2000 (first entry)

XX DE Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.

XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX OS Homo sapiens.

XX PN JP2000080100-A.

XX PD 21-MAR-2000.

XX PF 12-OCT-1998; 98JP-0304793.

XX PR 17-JUN-1998; 98JP-0188196.

XX PR 26-JUN-1998; 98JP-0196729.

XX PA (NISB ) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

XX DR N-PSDB; AAA13921.

XX PT A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone

Db 181 SGNQSVTEQSDKSTYSLSTLTKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 10  
AAW71876  
ID AAW71876 standard; Protein; 239 AA.  
XX  
AC AAW71876;  
XX  
DT 18-JAN-1999 (first entry)  
XX  
DE Anti-human Fas humanised antibody CH11 light chain VL-KY.  
XX  
KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;  
KW autoimmune disease; rheumatoid arthritis; therapy; human;  
KW antibody engineering.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= Sig\_peptide  
FT Protein 21..239  
FT /label= Mat\_protein  
FT Region 44..59  
FT /label= CDR1  
FT /note= "complementarity determining region 1 from  
FT CH11 light chain"  
FT Region 75..81  
FT /label= CDR2  
FT /note= "complementarity determining region 2 from  
FT CH11 light chain"  
FT Region 114..122  
FT /label= CDR3  
FT /note= "complementarity determining region 3 from  
FT CH11 light chain"  
XX  
EP866131-A2.  
XX  
XX 23-SEP-1998.  
XX  
XX 20-MAR-1998; 98EP-0302113.  
XX  
XX 21-MAR-1997; 97JP-0067938.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;  
PI Yonehara S;  
XX  
XX WPI: 1998-482965/42.  
DR N-PSDB; AAV61359.  
XX  
XX Production of anti-Fas protein humanised antibodies - for use in  
PT inducing apoptosis on Fas expressing cells in the treatment of  
PT autoimmune diseases, especially rheumatoid arthritis  
XX  
XX Claim 21; Page 94; 187pp; English.  
XX  
XX This is the amino acid sequence of a humanised anti-Fas antibody  
CC CH11 light chain, designated VL-KY. VL-KY is based on the light  
CC chain (see AAW71889) of murine anti-human Fas monoclonal antibody  
CC CH11. The humanised sequence was designed following selection of  
CC donor residues from CH11 to be grafted onto acceptor molecule  
CC RPM16410/C1. 4 light chain sequences (see AAW71876-79) have been  
CC designed, and each can be used in combination with either of 2  
CC heavy chain sequences (see AAW71880-81) to provide novel, claimed  
CC humanised CH11 IgM antibodies that lack a J chain. These humanised  
CC anti-human Fas antibodies are capable of inducing apoptosis in cells  
CC expressing Fas (e.g. synovocytes) and are useful in the treatment  
CC of autoimmune disease and chronic rheumatoid arthritis. DNA

CC sequences encoding the humanised antibodies are claimed, as are  
CC vectors such as pKappakY2-58 including the VL-KY nucleotide  
CC sequence (see AAV61359), and host cells such as Escherichia coli  
CC pKappakY2-58 (FERM BP-5861).  
XX  
SQ Sequence 239 AA;  
Query Match 89.4%; Score 1110; DB 19; Length 239;  
Best Local Similarity 89.5%; Pred. No. 2.4e-61;  
Matches 214; Conservative 10; Mismatches 15; Indels 0; Gaps 0;  
QY 1 MSLEPAQLGLLLCLVCGSSGEVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTPLSW 60  
Db 1 MRLEPAQLGLLLMLWPGSSGDVMTQSPSLPVLGQPASISCRSSKSLVHSGNTYLHW 60  
QY 61 YQKPGQPPRLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGYYFCQGGTRTP 120  
Db 61 YLQPGQSPKLLIYKVSNRFGVDPDRFSGSGSGTDFTLKISRVEAEDVGYYCSQSTHVP 120  
QY 121 PTFGGGTVKIKRTVAAPSVPFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
Db 121 PAFQGGTKVBIKRTVAAPSVPFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
QY 181 SGRSQESVTEQSDKSTYSLSTLTKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 239  
Db 181 SGRSQESVTEQSDKSTYSLSTLTKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 11  
AAB12913  
ID AAB12913 standard; Protein; 239 AA.  
XX  
XX AAB12913;  
XX  
DT 16-NOV-2000 (first entry)  
XX  
DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #78.  
XX  
KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
KW immunosuppression; autoimmune disease; treatment; rheumatism;  
KW anti-Fas antibody.  
XX  
OS Synthetic.  
XX  
XX JP2000154149-A.  
XX  
XX 06-JUN-2000.  
XX  
XX 17-SEP-1999; 99JP-0263984.  
XX  
XX 18-SEP-1998; 98JP-0264598.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX WPI: 2000-454476/40.  
DR N-PSDB; AAA78267.  
XX  
XX Anti-human Fas humanizing antibody-containing antirheumatic agents -  
PT  
XX Claim 1; Page 66-67; 109pp; Japanese.  
XX  
XX The present invention relates to antirheumatic agents which comprise as  
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
CC does not include a J segment, has apoptosis inducing activity, and  
CC consists of a light and heavy chain polypeptide produced synthetically.  
CC The agents of the invention exhibit antirheumatic and immunosuppressive  
CC activity and can be used to treat autoimmune diseases, especially  
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
CC binding properties. Included in the invention are nucleotide sequences  
CC of the IgM light and heavy chains (see AAB12913-B12918 and AAB12919), and  
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also



DT XX 16-NOV-2000 (first entry)  
 DE XX Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #80.  
 XX  
 KW Anti-rheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
 KW immunosuppression; autoimmune disease; treatment; rheumatism;  
 XX anti-Fas antibody.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2000154149-A.  
 XX  
 PD 06-JUN-2000.  
 XX  
 PF 17-SEP-1999; 99JP-0263984.  
 XX  
 PR 18-SEP-1998; 98JP-0264598.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2000-454476/40.  
 DR N-PSDB; AAA78268.  
 XX  
 PT Anti-human Fas humanizing antibody-containing antirheumatic agents -  
 XX  
 PS Claim 1; Page 68-69; 109pp; Japanese.  
 CC  
 CC The present invention relates to antirheumatic agents which comprise as  
 CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
 CC does not include a J segment, has apoptosis inducing activity, and  
 CC consists of a light and heavy chain polypeptide produced synthetically.  
 CC The agents of the invention exhibit antirheumatic and immunosuppressive  
 CC activity and can be used to treat autoimmune diseases, especially  
 CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
 CC binding properties. Included in the invention are nucleotide sequences  
 CC of the IgM light and heavy chains (see AAB12913-B12918 and AAB12919), and  
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
 CC AAB12902-A78206) and protein sequences (see AAB12908-B12910). Also  
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
 CC chains used in the invention are represented by sequences  
 CC AAB12913-A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AAA78277-A78318 and  
 CC AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AAA78321-A78334 and AAA78338-A78367. Primers  
 CC represented by sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in  
 CC the production of the agent of the invention.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 89.6%; Score 1113; DB 21; Length 239;  
 Best Local Similarity 90.0%; Pred. No. 1.6e-61;  
 Matches 215; Conservative 9; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 MSPLPAQLGLLLLCVPGSGGVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 Db 1 MRLPAQLGLLLMLVPGSGGDVMTQSPSLPVLTPGASISCRSSKSLVHSNGNTYLHW 60  
 QY 61 YQKPGQPPRLLIYKVNRSNDSGVDPDRFSGSGAGTDFTLKISAVEADVGVYFCGQGRTP 120  
 Db 61 YLQKPGQPKLLIYKVNRSNDSGVDPDRFSGSGAGTDFTLKISRVEADVGVYFCQSQTHP 120  
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQ 180  
 Db 121 PAFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQ 180  
 QY 181 SGNSQSVTEQDSKDYSLSTLTLKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239  
 Db 181 SGNSQSVTEQDSKDYSLSTLTLKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 9

AAB12915  
 ID AAB12915 standard; Protein; 239 AA.  
 XX  
 AC AAB12915;  
 XX  
 DT 16-NOV-2000 (first entry)  
 XX  
 DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #82.  
 XX  
 KW Anti-rheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
 KW immunosuppression; autoimmune disease; treatment; rheumatism;  
 KW anti-Fas antibody.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2000154149-A.  
 XX  
 PD 06-JUN-2000.  
 XX  
 PF 17-SEP-1999; 99JP-0263984.  
 XX  
 PR 18-SEP-1998; 98JP-0264598.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2000-454476/40.  
 DR N-PSDB; AAA78269.  
 XX  
 PT Anti-human Fas humanizing antibody-containing antirheumatic agents -  
 XX  
 PS Claim 1; Page 70-71; 109pp; Japanese.  
 CC  
 CC The present invention relates to antirheumatic agents which comprise as  
 CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
 CC does not include a J segment, has apoptosis inducing activity, and  
 CC consists of a light and heavy chain polypeptide produced synthetically.  
 CC The agents of the invention exhibit antirheumatic and immunosuppressive  
 CC activity and can be used to treat autoimmune diseases, especially  
 CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
 CC binding properties. Included in the invention are nucleotide sequences  
 CC of the IgM light and heavy chains (see AAB12913-B12918 and AAB12919), and  
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
 CC AAB12902-A78206) and protein sequences (see AAB12908-B12910). Also  
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
 CC chains used in the invention are represented by sequences  
 CC AAB12913-A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AAA78277-A78318 and  
 CC AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AAA78321-A78334 and AAA78338-A78367. Primers  
 CC represented by sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in  
 CC the production of the agent of the invention.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 89.6%; Score 1113; DB 21;  
 Best Local Similarity 90.0%; Pred. No. 1.6e-61;  
 Matches 215; Conservative 9; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 MSPLPAQLGLLLLCVPGSGGVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 Db 1 MRLPAQLGLLLMLVPGSGGDVMTQSPSLPVLTPGASISCRSSKSLVHSNGNTYLHW 60  
 QY 61 YQKPGQPPRLLIYKVNRSNDSGVDPDRFSGSGAGTDFTLKISAVEADVGVYFCGQGRTP 120  
 Db 61 YLQKPGQPKLLIYKVNRSNDSGVDPDRFSGSGAGTDFTLKISRVEADVGVYFCQSQTHP 120  
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQ 180  
 Db 121 PAFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQ 180  
 QY 181 SGNSQSVTEQDSKDYSLSTLTLKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239  
 Db 181 SGNSQSVTEQDSKDYSLSTLTLKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

XX Claim 23; Page 96-97; 187pp; English.

PS This is the amino acid sequence of a humanised anti-Fas antibody

XX CH11 light chain, designated VL-KF. VL-KF is based on the light

CC chain (see AAW71899) of murine anti-human Fas monoclonal antibody

CC CH11. The humanised sequence was designed following selection of

CC donor residues from CH11 to be grafted onto acceptor molecule

CC RPM16410/CL. 4 Light chain sequences (see AAW71876-79) have been

CC designed, and each can be used in combination with either of 2

CC heavy chain sequences (see AAW71880-81) to provide novel, claimed

CC humanised CH11 IGM antibodies that lack a J chain. These humanised

CC anti-human Fas antibodies are capable of inducing apoptosis in cells

CC expressing Fas (e.g. synovocytes) and are useful in the treatment

CC of autoimmune disease and chronic rheumatoid arthritis. DNA

CC sequences encoding the humanised antibodies are claimed, as are

CC vectors such as pKappaKF2-19 including the VL-KF nucleotide

CC sequence (see AAV61360) and host cells such as Escherichia coli

CC pKappaKF2-19 (FERM BP-5860).

XX Sequence 239 AA;

Query Match 89.6%; Score 1113; DB 19; Length 239;

Best Local Similarity 90.0%; Pred. No. 1.6e-61;

Matches 215; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSSGEVVMTPSLPITGEPASISCRSSQSLKHSNGDTFLSW 60

DB 1 MRLPAQLGLLLMLWVPGSSGDVVMTPSLPVLGQPASISCRSSKSLVHSNGNTYLHW 60

QY 61 YQKPGQPPRLLIYKVNRSRSGVDPDFSGSGAGTDTLTKISAVEADVGYYFCQGTTRP 120

DB 61 YLQKPGQPKLLIYKVNRSRSGVDPDFSGSGAGTDTLTKISAVEADVGYYFCQSTHVP 120

QY 121 PTFGGGTKEIKRTVAAPSVPFIPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180

DB 121 PAFGGGTKEIKRTVAAPSVPFIPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180

QY 181 SGNSQESVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

DB 181 SGNSQESVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 7

AAW71878

ID AAW71878 standard; Protein; 239 AA.

AC AAW71878;

XX

DT 18-JAN-1999 (first entry)

XX Anti-human Fas humanised antibody CH11 light chain VL-RY.

XX

KW Humanised antibody; Fas; CH11; monoclonal antibody; MAB; apoptosis;

KW autoimmune disease; rheumatoid arthritis; therapy; human;

XX antibody engineering.

XX Homo sapiens.

OS Synthetic.

XX

PH Key Location/Qualifiers

FT Peptide 1..20

FT /label= sig\_peptide

FT Protein 21..239

FT /label= Mat\_protein

FT Region 44..59

FT /label= CDR1

FT /note= "complementarity determining region 1 from

FT CH11 light chain"

FT

FT Region 75..81

FT /label= CDR2

FT /note= "complementarity determining region 2 from

FT CH11 light chain"

FT

FT Region 114..122

PS /label= CDR3

FT /note= "complementarity determining region 3 from

FT CH11 light chain"

XX

EP866131-A2.

XX

23-SEP-1998.

XX

20-MAR-1998; 98EP-0302113.

XX

21-MAR-1997; 97JP-0067938.

XX

(SANY ) SANKYO CO LTD.

PA

Haruyama H, Nakahara K, Serizawa N, Takahashi T;

PI Yonehara S;

XX

WPI: 1998-482965/42.

DR N-PSDB; AAV61362.

XX

Production of anti-Fas protein humanised antibodies - for use in

PT inducing apoptosis on Fas expressing cells in the treatment of

PT autoimmune diseases, especially rheumatoid arthritis

XX

Claim 25; Page 99; 187pp; English.

XX

This is the amino acid sequence of a humanised anti-Fas antibody

CC CH11 light chain, designated VL-RY. VL-RY is based on the light

CC chain (see AAW71889) of murine anti-human Fas monoclonal antibody

CC CH11. The humanised sequence was designed following selection of

CC donor residues from CH11 to be grafted onto acceptor molecule

CC RPM16410/CL. 4 Light chain sequences (see AAW71876-79) have been

CC designed, and each can be used in combination with either of 2

CC heavy chain sequences (see AAW71880-81) to provide novel, claimed

CC humanised CH11 IGM antibodies that lack a J chain. These humanised

CC anti-human Fas antibodies are capable of inducing apoptosis in cells

CC expressing Fas (e.g. synovocytes) and are useful in the treatment

CC of autoimmune disease and chronic rheumatoid arthritis. DNA

CC sequences encoding the humanised antibodies are claimed, as are

CC vectors such as pKappaRY2-10 including the VL-RY nucleotide

CC sequence (see AAV61361), and host cells such as Escherichia coli

CC pKappaRY2-10 (FERM BP-5859).

XX

Sequence 239 AA;

Query Match 89.6%; Score 1113; DB 19; Length 239;

Best Local Similarity 90.0%; Pred. No. 1.6e-61;

Matches 215; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSLPAQLGLLLCVPGSSGEVVMTPSLPITGEPASISCRSSQSLKHSNGDTFLSW 60

DB 1 MRLPAQLGLLLMLWVPGSSGDVVMTPSLPVLGQPASISCRSSKSLVHSNGNTYLHW 60

QY 61 YQKPGQPPRLLIYKVNRSRSGVDPDFSGSGAGTDTLTKISAVEADVGYYFCQGTTRP 120

DB 61 YLQKPGQPKLLIYKVNRSRSGVDPDFSGSGAGTDTLTKISAVEADVGYYFCQSTHVP 120

QY 121 PTFGGGTKEIKRTVAAPSVPFIPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180

DB 121 PAFGGGTKEIKRTVAAPSVPFIPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180

QY 181 SGNSQESVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

DB 181 SGNSQESVTEQDSKDYSLSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8

AAW712914

ID AAW712914 standard; Protein; 239 AA.

XX

AC AAW712914;

XX

QY 61 YQKPGOPRLLIYKVNRSQVDFRFGSGAGTDFTLKISAVEAEDVGVFCGGTTRTP 120  
 DB 61 YLQKPGOPRLLIYKVNRSQVDFRFGSGAGTDFTLKISAVEAEDVGVFCGGTTRTP 120  
 QY 121 PTEGGTKEIKRTVAASVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180  
 DB 121 PARQGGTKEIKRTVAASVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180  
 QY 181 SGNSQSVTEQDSKDYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 239  
 DB 181 SGNSQSVTEQDSKDYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 239  
 RESULT 5  
 AAB12916  
 ID AAB12916 standard; Protein; 239 AA.  
 XX  
 AC AAB12916;  
 DT 16-NOV-2000 (first entry)  
 DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #84.  
 XX  
 KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
 KW immunosuppression; autoimmune disease; treatment; rheumatism;  
 KW anti-Fas antibody.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2000154149-A.  
 XX  
 PD 06-JUN-2000.  
 XX  
 PF 17-SEP-1999; 99JP-0263984.  
 XX  
 PR 18-SEP-1998; 98JP-0264598.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2000-454476/40.  
 XX  
 DR N-PSDB; AAA78270.  
 XX  
 PT Anti-human Fas humanizing antibody-containing antirheumatic agents -  
 XX  
 PS Claim 1; Page 72-73; 109pp; Japanese.  
 CC The present invention relates to antirheumatic agents which comprise as  
 CC active ingredient an immunoglobulin M (IgM) protein. The IgM protein  
 CC does not include a J segment, has apoptosis inducing activity and  
 CC consists of a light and heavy chain polypeptide produced synthetically.  
 CC The agents of the invention exhibit antirheumatic and immunosuppressive  
 CC activity and can be used to treat autoimmune diseases, especially  
 CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
 CC binding properties. Included in the invention are nucleotide sequences  
 CC of the IgM light and heavy chains (see AAB12916-A78272) and the  
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
 CC nucleotide sequences of the humanised anti-human Fas Ig ChII (see  
 CC AAB12902-A78206) and protein sequences (see AAB12908-B12910). Also  
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
 CC chains used in the invention are represented by sequences  
 CC AAB12913-A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AAB12913-A78318 and  
 CC AAB12913-A78317, while humanised anti-Fas Ig DNA sequencing primers are  
 CC represented by sequences AAB12913-A78334 and AAB12913-A78367. Primer  
 CC sequences AAB12907-A78212 are specific for murine Ig DNA, and are used in  
 CC the production of the agent of the invention.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 89.9%; Score 1116; DB 21; Length 239;  
 Best Local Similarity 90.4%; Pred. No. 1e-61;

Matches 216; Conservative 8; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 MSIPAGLLGLLLCVPGSSGEVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 DB 1 YLQKPGOPRLLIYKVNRSQVDFRFGSGAGTDFTLKISAVEAEDVGVFCGGTTRTP 120  
 QY 61 YQKPGOPRLLIYKVNRSQVDFRFGSGAGTDFTLKISAVEAEDVGVFCGGTTRTP 120  
 DB 61 YLQKPGOPRLLIYKVNRSQVDFRFGSGAGTDFTLKISAVEAEDVGVFCGGTTRTP 120  
 QY 121 PTEGGTKEIKRTVAASVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180  
 DB 121 PARQGGTKEIKRTVAASVFIIPPDSDEQLKSGTASVCLNNFYPREAKVQWVDNALQ 180  
 QY 181 SGNSQSVTEQDSKDYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 239  
 DB 181 SGNSQSVTEQDSKDYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 239  
 RESULT 6  
 AAW71877  
 ID AAW71877 standard; Protein; 239 AA.  
 XX  
 AC AAW71877;  
 DT 18-JAN-1999 (first entry)  
 DE Anti-human Fas humanised antibody CH11 light chain VL-KF.  
 XX  
 KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;  
 KW autoimmune disease; rheumatoid arthritis; therapy; human;  
 KW antibody engineering.  
 XX  
 OS Homo sapiens.  
 XX  
 PN Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT Peptide 1..20 /label= Sig\_peptide  
 FT Protein 21..239 /label= Mat\_protein  
 FT Region 44..59 /label= CDR1  
 FT /note= "complementarity determining region 1 from  
 FT CH11 light chain"  
 FT Region 75..81 /label= CDR2  
 FT /note= "complementarity determining region 2 from  
 FT CH11 light chain"  
 FT Region 114..122 /label= CDR3  
 FT /note= "complementarity determining region 3 from  
 FT CH11 light chain"  
 XX  
 PN EP866131-A2.  
 XX  
 PD 23-SEP-1998.  
 XX  
 PF 20-MAR-1998; 98EP-0302113.  
 XX  
 PR 21-MAR-1997; 97JP-0067938.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 XX  
 XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;  
 PI Yonehara S;  
 XX WPI; 1998-482965/42.  
 DR N-PSDB; AAV61360.  
 XX  
 PT Production of anti-Fas protein humanised antibodies - for use in  
 PT inducing apoptosis on Fas expressing cells in the treatment of  
 PT autoimmune diseases, especially rheumatoid arthritis

XX PD 29-NOV-2001.  
 XX PF 22-MAY-2001; 2001WO-US16364.  
 XX PR 22-MAY-2000; 2000US-0576424.  
 XX PA (IDEC-) IDEC PHARM CORP.  
 XX PI Anderson DR, Hanna N, Brams P;  
 XX PR WPI; 2002-089895/12.  
 XX DR N-PSDB; AAS17244.  
 XX PT Use of monoclonal antibody which specifically binds to B7.1 antigen  
 FT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, as  
 FT treating cancer, graft-vs-host disease and autoimmune disease such as  
 FT allergy -  
 XX PS Example 8; Fig 4a; 89pp; English.  
 XX CC The present invention relates to a new use of a monoclonal antibody  
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen  
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is  
 CC useful for treating diseases such as B cell cancer, lymphoma, a  
 CC cancer where B cells promote the growth and/or metastasis of tumours,  
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as  
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosis,  
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic  
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis  
 CC or graft-vs-host disease. The antibody is useful for immunosuppression  
 CC in a human or animal and for treating or preventing resistance to or  
 CC rejection of transplanted organ or tissue for treating proliferative  
 CC and hyperproliferative diseases, for treating reversible obstructive  
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's  
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,  
 CC rhinitis and eczema, and other types of allergies. The present protein  
 CC sequence represents the light chain of 786, a primatised antibody  
 CC used in the invention to induce apoptosis.  
 XX SQ Sequence 239 AA;

Query Match 100.0%; Score 1242; DB 23; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-69;  
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSPLAQLGLLLLCVPGSGEVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 Db 1 MSPLAQLGLLLLCVPGSGEVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 Qy 61 YQKPGQPRLIIYKVNRSNDSGVPDRFSGSGAGTDFTLKISAVEAEVGVVFCQGRTRP 120  
 Db 61 YQKPGQPRLIIYKVNRSNDSGVPDRFSGSGAGTDFTLKISAVEAEVGVVFCQGRTRP 120  
 Qy 121 PTFGGGTVEIKRTVAAPSVEFPDPSDQSLKSGTASVVCLLNFFPREAKVQWKNALQ 180  
 Db 121 PTFGGGTVEIKRTVAAPSVEFPDPSDQSLKSGTASVVCLLNFFPREAKVQWKNALQ 180  
 Qy 181 SGNQSEVTEODSKDSTYSLSSTLTSLRADYKHKVACEVTHQGLSPVTKSNRQEC 239  
 Db 181 SGNQSEVTEODSKDSTYSLSSTLTSLRADYKHKVACEVTHQGLSPVTKSNRQEC 239

## RESULT 4

AAW71879

ID AAW71879 standard; Protein; 239 AA.

XX AC AAW71879;

XX DT 18-JAN-1999 (first entry)

XX DE Anti-human Fas humanised antibody CH11 light chain VL-RF.  
 XX

XX KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;  
 KW autoimmune disease; rheumatoid arthritis; therapy; human;  
 XX antibody engineering.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX FH Location/Qualifiers  
 FT Key 1..20  
 FT Peptide /label= Sig\_peptide  
 FT Protein 21..239  
 FT Region /label= Mat\_protein  
 FT 44..59  
 FT /label= CDR1  
 FT /notes= "complementarity determining region 1 from  
 FT CH11 light chain"  
 FT Region 75..81  
 FT /label= CDR2  
 FT /notes= "complementarity determining region 2 from  
 FT CH11 light chain"  
 FT Region 114..122  
 FT /label= CDR3  
 FT /notes= "complementarity determining region 3 from  
 FT CH11 light chain"  
 XX EP866131-A2.  
 XX 23-SEP-1998.  
 XX 20-MAR-1998; 98EP-0302113.  
 XX 21-MAR-1997; 97JP-0067938.  
 XX (SANY) SANKYO CO LTD.  
 XX Hanyama H, Nakahara K, Serizawa N, Takahashi T;  
 XX Itonohara S;  
 XX WPI; 1998-482965/42.  
 XX N-PSDB; AAV61362.  
 XX Production of anti-Fas protein humanised antibodies - for use in  
 XX inducing apoptosis on Fas expressing cells in the treatment of  
 XX autoimmune diseases, especially rheumatoid arthritis  
 XX Claim 27; Page 101-102; 187pp; English.  
 XX This is the amino acid sequence of a humanised anti-Fas antibody  
 XX CH11 light chain, designated VL-RF. VL-RF is based on the light  
 XX chain (see AAW71889) of murine anti-human Fas monoclonal antibody  
 XX CH11. The humanised sequence was designed following selection of  
 XX donor residues from CH11 to be grafted onto acceptor molecule  
 XX rPM16410'CL. 4 Light chain sequences (see AAW71876-79) have been  
 XX designed, and each can be used in combination with either of 2  
 XX heavy chain sequences (see AAW71880-81) to provide novel, claimed  
 XX humanised CH11 IGM antibodies that lack a J chain. These humanised  
 XX anti-human Fas antibodies are capable of inducing apoptosis in cells  
 XX expressing Fas (e.g. synovocytes) and are useful in the treatment  
 XX of autoimmune disease and chronic rheumatoid arthritis. DNA  
 XX sequences encoding the humanised antibodies are claimed, as are  
 XX vectors such as pKappapR2-52 including the VL-RF nucleotide  
 XX sequence (see AAV61362), and host cells such as Escherichia coli  
 XX pKappapR2-52 (FERM BP-5862).  
 XX SQ Sequence 239 AA;  
 Query Match 89.9%; Score 1116; DB 19; Length 239;  
 Best Local Similarity 90.4%; Pred. No. 1e-61;  
 Matches 216; Conservative 8; Mismatches 15; Indels 0; Gaps 0;  
 Qy 1 MSPLAQLGLLLLCVPGSGEVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60  
 Db 1 MSPLAQLGLLLLCVPGSGEVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60

DR N-PSDB; AAT62511.  
 XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -  
 PT useful for treating autoimmune disease or graft-versus-host disease  
 PT  
 PS Claim 8; Fig 9A; 81pp; English.  
 XX  
 CC 2 Polypeptides (AAW01819 and AAW01820) respectively comprise primatised  
 CC forms of the light and heavy chains of cynomolgus monkey anti-human  
 CC B7.1 antigen monoclonal antibody 7B6. Cloned 7B6 light and heavy  
 CC variable genes (see also AAT62511 and AAT13847) are inserted into  
 CC an expression vector (pref. NEOSPLA) which contains human light and  
 CC heavy chain constant region genes to allow prodn. of the primatised  
 CC antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1  
 CC antibodies have also been produced (see also AAW01817-19 and  
 CC AAW01821-22). The primatised antibodies inhibit the B7:CD28 pathway,  
 CC making them useful immunosuppressants for the treatment of  
 CC autoimmune disorders and graft-versus-host disease.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 100.0%; Score 1242; DB 18; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-69;  
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSLPAQLGLLLCVPGSGGEVWVTQSPSLPITFGEPASISCRSSQSLKHNGDTFLSW 60  
 DB 1 MSLPAQLGLLLCVPGSGGEVWVTQSPSLPITFGEPASISCRSSQSLKHNGDTFLSW 60  
 QY 61 YQKPGOPRLIYIKVNRDGVDPFSGSGAGDTFTLKISAVEAEVGVYFCGGGTRTP 120  
 DB 61 YQKPGOPRLIYIKVNRDGVDPFSGSGAGDTFTLKISAVEAEVGVYFCGGGTRTP 120  
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180  
 DB 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180  
 QY 181 SGNQSESVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239  
 DB 181 SGNQSESVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239  
 RESULT 2  
 AAW63762  
 ID AAW63762 standard; Protein; 239 AA.  
 AC AAW63762;  
 XX  
 XX 29-SEP-1998 (first entry)  
 DT  
 DE Macaque primatised 7B6 light chain protein.  
 KW Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;  
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;  
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;  
 KW immunogen; anti-idiotype reagent; interleukin-2; Igg; immunoglobulin G;  
 XX T cell proliferation.  
 XX  
 OS Macaca fascicularis.  
 XX  
 PN WO9819706-A1.  
 XX  
 PD 14-MAY-1998.  
 XX  
 XX 29-OCT-1997; 97WO-US19906.  
 XX  
 XX 08-NOV-1996; 96US-0746361.  
 XX  
 PA (IDEC-) IDEC PHARM CORP.  
 XX  
 PI Anderson DR, Brans P, Hanna N;  
 XX  
 XX WPI; 1998-286f01/25.

DR N-PSDB; AAV35486.  
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and  
 PT inhibiting binding to CD28 - useful as specific immunosuppressants  
 PT for treating diseases that involve interactions between T and B  
 PT cells, e.g. graft rejection or tumours  
 XX  
 PS Example 7; Fig 4a; 87pp; English.  
 XX  
 CC This sequence represents a primatised form of the antibody 7B6 light  
 CC chain from macaque. This sequence is used in a method which studies new  
 CC monoclonal antibodies (MAB's) that bind selectively to B7.1 (CD80) or to  
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such  
 CC MAB's are specific immunosuppressants for treatment of diseases involving  
 CC T cell/B cell interactions, particularly autoimmune disease, specifically  
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type  
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,  
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.  
 CC host diseases, B cell lymphoma, infections (including by human immune  
 CC deficiency virus) or inflammatory disease and tumours. Optionally the  
 CC MAB can be conjugated to a drug or toxin. MAB's, or their fragments, can  
 CC also be used as imaging agents and as vaccines or immunogens to develop  
 CC anti-idiotype reagents. MAB's are optionally combined with other proteins  
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions  
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits  
 CC production of interleukin-2 (IL-2), T cell proliferation and  
 CC antigen-specific immunoglobulin G (IgG) responses.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 100.0%; Score 1242; DB 19; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-69;  
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSLPAQLGLLLCVPGSGGEVWVTQSPSLPITFGEPASISCRSSQSLKHNGDTFLSW 60  
 DB 1 MSLPAQLGLLLCVPGSGGEVWVTQSPSLPITFGEPASISCRSSQSLKHNGDTFLSW 60  
 QY 61 YQKPGOPRLIYIKVNRDGVDPFSGSGAGDTFTLKISAVEAEVGVYFCGGGTRTP 120  
 DB 61 YQKPGOPRLIYIKVNRDGVDPFSGSGAGDTFTLKISAVEAEVGVYFCGGGTRTP 120  
 QY 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180  
 DB 121 PTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQ 180  
 QY 181 SGNQSESVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239  
 DB 181 SGNQSESVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 239  
 RESULT 3  
 AAV1540  
 ID AAV1540 standard; Protein; 239 AA.  
 XX  
 XX AAV1540;  
 XX  
 XX 12-MAR-2002 (first entry)  
 DT  
 DE Protein sequence of primatised form of the light chain of 7B6 antibody.  
 KW Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;  
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;  
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;  
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;  
 KW graft-vs-host disease; immunosuppression; organ rejection;  
 KW interleukin-2; IL-2; mutant; mutein.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Macaca sp.  
 OS Synthetic.  
 XX  
 PN WO200189567-A1.

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 25, 2003, 09:06:23 ; Search time 24.5816 Seconds  
(without alignments)  
1295.559 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSLPAQLGLLLCPVSSG.....EVTHQGLSSPTKSFNRGEC 239

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 101002:\*

1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
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11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
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13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
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20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	239	18 AAW01819	Primates anti-hu
2	1242	100.0	239	19 AAW63762	Macaque primatized
3	1242	100.0	239	23 AAW11540	Protein sequence o
4	1116	89.9	239	19 AAW71879	Anti-human Fas hum
5	1116	89.9	239	21 AAB12916	Anti-human Fas hum
6	1113	89.6	239	19 AAW71877	Anti-human Fas hum
7	1113	89.6	239	19 AAW71878	Anti-human Fas hum
8	1113	89.6	239	21 AAB12914	Anti-human Fas hum
9	1113	89.6	239	21 AAB12915	Anti-human Fas hum
10	1110	89.4	239	19 AAW71876	Anti-human Fas hum

11	1110	89.4	239	21 AAB12913	Anti-human Fas imm
12	1083	87.2	239	21 AAY82615	Human PTHrP monocl
13	1065	85.7	239	21 AAY82611	Human PTHrP monocl
14	1063	85.6	239	21 AAY82610	Human PTHrP monocl
15	1063	85.6	239	21 AAY82617	Human PTHrP monocl
16	1061	85.4	239	21 AAY82614	Human PTHrP monocl
17	1057	85.1	239	21 AAY82616	Human PTHrP monocl
18	1052.5	84.7	238	18 AAW14942	3F4 Human IgG4 exp
19	1052.5	84.7	238	18 AAW14937	Murine anti-porcine
20	1050	84.5	239	21 AAY82613	Human PTHrP monocl
21	1044	84.1	239	21 AAY82612	Human PTHrP monocl
22	1042	83.9	241	21 AAY96303	Human IGFAM-15 imm
23	1038.5	83.6	238	22 AAU07744	Humanised monocl
24	1037.5	83.5	238	17 AAR93554	Monoclonal antiod
25	1032	82.3	239	21 AAU77298	Protein #1 in inve
26	1018	82.0	239	21 AAY82618	Human PTHrP monocl
27	1016	81.8	239	21 AAY82619	Human PTHrP monocl
28	1007	81.1	238	22 AAB72231	Humanised 323/A3 (
29	1007	81.1	238	22 AAB72233	Humanised 323/A3 (
30	1007	81.1	238	22 AAB72235	Humanised 323/A3 (
31	992.5	79.9	220	22 AAB12714	Human recombinant
32	978	78.7	241	13 AAR28809	Vector pMDR1007.
33	976.5	78.6	238	19 AAW83034	Anti-Fas humanised
34	976.5	78.6	238	21 AAB14777	Humanised anti-Fas
35	976.5	78.6	238	21 AAW90927	Humanised HFE7A de
36	976.5	78.6	238	23 ABB74896	Humanised anti-Fas
37	976.5	78.6	238	23 ABB74896	Humanised anti-Fas
38	976.5	78.6	242	16 AAR66323	Chimeric 6G4.2.5.1
39	976	78.6	242	18 AAW42323	Murine variable re
40	976	78.6	242	18 AAW31580	Chimeric anti IL-8
41	976	78.6	242	18 AAW23790	Chimeric monoclon
42	976	78.6	242	19 AAW69311	Anti-IL-8 mouse-hu
43	976	78.6	242	19 AAW40126	Chimeric Mab 6G4.2
44	976	78.6	242	19 AAW33745	Chimeric anti IL-8
45	976	78.6	242	19 AAW33745	

#### ALIGNMENTS

RESULT 1  
AAW01819  
ID AAW01819 standard; Protein; 239 AA.  
XX AC AAW01819;  
XX DT 25-MAY-1997 (first entry)  
XX DE Primatised anti-human B7.1 antigen antibody 7B6 light chain.  
XX KW Monoclonal antibody; cynomolgus monkey; macaque; 7B6;  
XX KW Primatised antibody; B7 antigen; CD28; immunosuppressive;  
XX KW autoimmune disease; idiopathic thrombocytopenia purpura;  
XX KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;  
XX KW type 1 diabetes mellitus; graft versus host disease;  
XX KW hetero-hybridoma; transfectoma.  
XX OS Chimeric Macaca cynomolgus;  
XX OS Chimeric Homo sapiens.  
XX PN WO9640878-A1.  
XX PD 19-DEC-1996.  
XX PF 06-JUN-1996; 96WO-US10053.  
XX PR 07-JUN-1995; 95US-0487550.  
XX PA (IDEC-) IDEC PHARM CORP.  
XX PI Anderson DR, Brams P, Hanna N, Shestowsky WS;  
XX WP1; 1997-108638/10.

Hypothetical 24.9 kDa protein.  
DE Homo sapiens (Human)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TONSIL;  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC020298; AAH2098.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig.c1.  
DR InterPro; IPR003006; Ig.MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00409; Ig\_2.  
DR SMART; SM00407; Igc1; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
KW Hypothetical protein\_1.  
SQ SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;  
  
Query Match 35.2%; Score 437.5; DB 4; Length 237;  
Best Local Similarity 42.4%; Pred. No. 3.6e-33;  
Matches 101; Conservative 44; Mismatches 80; Indels 13; Gaps 8;  
  
QY 7 LIGLLLLCVPGSSGEVMTQSPLSLPITPGEPAISICRSQSLKHSNGDTFLSWYQKPG 66  
DB 7 LITLLAHT-GSWAQSVLTQPP-SVSGAPGQRTVITCTGSSSNIGAGYD--VHWYQQLPG 62  
  
QY 67 QPRLIYKVSNRDGVDPDRFSGSGAGTDTLTKISAVEAEDVGVFYFCGQTRTPPTF 123  
DB 63 TAPKLLIYGNRNRPSPGVDPDRFSGSKSGTASLAITGLQAEDEADYYCQSYDSSLGSGV 122  
  
QY 124 GGGTKVEI-KRTVAAPSVFIPTPPDEQLKSGTASVCLNNFYPREAKVQKVDNA-LQS 181  
DB 123 GGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKA 182  
  
QY 182 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 239  
DB 183 G--VETTTFSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVAPTEC 236  
  
Search completed: March 29, 2003, 09:14:38  
Job time : 22.6765 secs

Hypothetical 24.9 kDa protein.  
DE Homo sapiens (Human)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TONSIL;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC020233; AAH20233.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig.c1.  
DR InterPro; IPR003006; Ig.MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00409; Ig\_2.  
DR SMART; SM00407; Igc1; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
KW Hypothetical protein\_1.  
SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

RESULT 15  
Q8WUK4  
ID Q8WUK4 PRELIMINARY; PRT; 237 AA.  
AC Q8WUK4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical 24.9 kDa protein.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TONSIL;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC020233; AAH20233.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig.c1.  
DR InterPro; IPR003006; Ig.MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_2.  
DR SMART; SM00409; Ig\_2.  
DR SMART; SM00407; Igc1; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
KW Hypothetical protein\_1.  
SQ SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 51.4%; Score 638.5; DB 11; Length 214;
Best Local Similarity 53.9%; Pred. No. 3.7e-52;
Matches 118; Conservative 42; Mismatches 54; Indels 5; Gaps 1;

QY 21 EVVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80
DB 1 DIQUTQSPSSWASLGERVITTCASQDI-----NSVLSWFQKPKGKPTLIYRANRLV 55

QY 81 SGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCQGQTRTPP-TFGGGTKVEIKR 140
DB 56 DGVPSRFSGSGGDYSLTISLEVEDWGIYCLQYDEFFTFGSGTKLEIKRAAAPT 115

QY 141 FIPPPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYS 200
DB 116 SIFPPSEQLTSGTSGASVVCFLNNFYPRDINKVKIDGSRQNGVLNSWTDQDSKDSTYS 175

QY 201 SSTLTLSKADYEKHKVACETVTHOGLSSPVTKSFNRGEC 239
DB 176 SSTLTLTNDEYERHNSYTCETATHKTSIPVLCFNRNEC 214

RESULT 12
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035034; AAD56270.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 114
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 37.2%; Score 462.5; DB 4; Length 114;
Best Local Similarity 78.9%; Pred. No. 5.7e-36;
Matches 90; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

QY 21 EVVMTQSPSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80
DB 1 DVVMTQSPSLPVLTRQPAISCRSSQSPVYSDGNTLNNWFQRPQSPRRLIIYKVSNRD 60

QY 81 SGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFCQGQTRTPP-TFGGGTKVEIKR 133
DB 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYCMQGTTHWPWTFGGTKVEIKR 114

RESULT 13
Q8TEC9 PRELIMINARY; PRT; 233 AA.
AC Q8TEC9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 24.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022823; AAH22823.1; -.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;

Query Match 37.1%; Score 460.5; DB 4; Length 233;
Best Local Similarity 42.7%; Pred. No. 2.4e-35;
Matches 103; Conservative 45; Mismatches 70; Indels 23; Gaps 9;

QY 7 LLGLLLLCVPGSSGEVMTQSPSLPITPGEPAISCRSSQSLKHSNGDT---FLSWYQ 62
DB 7 LLPLTLCT-GSEASVELTQPP-SVSVSPGQTARITC-----SGDALPKQAYVWQ 55

QY 63 QKPGQPPRLIIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEAEDVGVYFC--GGGTTP 120
DB 56 QKPGQAPVLVIYKDNRPSPGIPERFSGSSGTTVLTITSGVQAEDEADYYCOSADSSGT 115

QY 121 PTFGGTKVEI-KRTVAAPSVFIRPPDEQLKSGTASVVCLLNNFYPREAKVQKVDNA- 178
DB 116 WYFGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSP 175

QY 179 LQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGE 238
DB 176 VKAG--VETTTFSKQSNKNKYAASSVLSLTPEQWKSHKSYSCQVTHEG--STVEKTVAPTE 231

QY 239 C 239
DB 232 C 232

RESULT 14
Q8WTU6 PRELIMINARY; PRT; 237 AA.
AC Q8WTU6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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QY 181 SGNQSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239
Db 176 QNGVLNSWTDQDSKDYSSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNREC 234

RESULT 8
Q91W12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD583FEF CRC64;

Query Match
Best Local Similarity 53.1%; Score 667; DB 11; Length 235;
Matches 128; Conservative 37; Mismatches 68; Indels 8; Gaps 2;

QY 1 MSIPALLGLLL--CVPSSGEVMTQSPLSLPITPGEPAISCRSSQSLKHSNGDTFL 58
Db 1 MDPQVIFGLLSAVIISRGQIVLTQSPALMSASPGERVMTCSASSVSH-----M 54

QY 59 SWYQKFGPPRLIIYKVNRSQVDPDRFSGSGAGDTFTLKISAVEADVGVYFCQGTR 118
Db 55 HWYQKSGTSKREWIYDTFKLNSGVPDRFSGSGSTSYSLTISNMEADVATYYCQNSR 114

QY 119 TPTFGGGTKEIKRTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVNA 178
Db 115 NPPTFGVTKLELKRADAAPTIVSIFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGS 174

QY 179 LOSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGE 238
Db 175 ERQNGVLNSWTDQDSKDYSSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNRE 234

QY 239 C 239
Db 235 C 235

RESULT 9
Q8R028
ID Q8R028 PRELIMINARY; PRT; 234 AA.
AC Q8R028;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028540; AAH28540.1; -.
KW Hypothetical protein.

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SQ SEQUENCE 234 AA; 25702 MW; 148377F9C1CD0A8E CRC64;

Query Match
Best Local Similarity 52.9%; Score 656.5; DB 11; Length 234;
Matches 128; Conservative 30; Mismatches 72; Indels 5; Gaps 1;

QY 5 AQLGLLLCVPSSGEVMTQSPLSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQOK 64
Db 5 APLSLLLCVDSDSRAETTVTQSPASLSVATGKVTIRCTITSDI-----DDDMNMYQOK 59

QY 65 PGQPPRLIIYKVNRSQVDPDRFSGSGAGDTFTLKISAVEADVGVYFCQGTRTPPTFG 124
Db 60 PGEPPKLLISEGNTLRPGVPSRFSSSGSGTDFVFTTENTLSEADVADYICLQSDNMPITFG 119

QY 125 GGTKEIKRTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVNALOSGNS 184
Db 120 AGTKLELKRADAAPTIVSIFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGV 179

QY 185 QESVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239
Db 180 LNSWTDQDSKDYSSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNREC 234

RESULT 10
Q91WS9
ID Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match
Best Local Similarity 52.8%; Score 655.5; DB 11; Length 233;
Matches 127; Conservative 34; Mismatches 63; Indels 5; Gaps 1;

QY 11 LLLCVPSSGEVMTQSPLSLPITPGEPAISCRSSQSLKHSNGDTFLSWYQOKGQPPR 70
Db 10 LLLCFQGSRCDIQMTQTSLSASLGRVITISCSGSGIAN-----VLNMYQOKPDGTVK 64

QY 71 LLIIYKVNRSQVDPDRFSGSGAGDTFTLKISAVEADVGVYFCQGTRTPPTFGGKTVE 130
Db 65 LLIIYTSLSHSGVPSRFSGSGSGTSDYSLTISNLEPEDIAITYCQYRILPFTWTFGGTKLE 124

QY 131 IKRTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVNALOSGNSQSVTE 190
Db 125 IKRADAAPTIVSIFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWD 184

QY 191 QDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239
Db 185 QDSKDYSLSTLTITKDEYERHNSYTCEATHKTSPIVKSFNREC 233

RESULT 11
Q9RIAS
ID Q9RIAS PRELIMINARY; PRT; 214 AA.
AC Q9RIAS;

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Db 61 YLQKPGSQQLLIYVSNRFGVDPDRFSGSGGTDFTLKISRVEADLGVYFCQSNHLP 120
Qy 121 PTFGGGKVEIKRTVAAPSVFIPPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQ 180
Db 121 YTFGGGKLEIKRADAAPTVSIFFPPSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSR 180
Qy 181 SGNQSQSVTEQDSKDYSLSSLTLSKADYKHVKYACVETHQGLSSPVTKSFNRGEC 239
Db 181 QNGVLNSWTDQDSKDYSSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREK 239

RESULT 5
Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAH19474.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2A9F CRC64;

Query Match 55.7%; Score 691.5; DB 11; Length 234;
Best Local Similarity 54.0%; Pred. No. 4.2e-57;
Matches 129; Conservative 44; Mismatches 61; Indels 5; Gaps 1;

Qy 1 MSLPAQLGLLLLCVPGSSGEVVMVTPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MSVPTQVLGLLLCLTGARCDIQLTSPASLSASVGETVITCRASENIY-----SYLAW 55

Qy 61 YQKPGQPRLIIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEADGVYFCQGTTRP 120
Db 56 YQKQKSPQLLYVNAKTLADGVPSRFGSRGTQSLKINSIQPEDFGSYQCQHSZIP 115

Qy 121 PTFGGGKVEIKRTVAAPSVFIPPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQ 180
Db 116 FTFGSGTKLEIKRADAAPTVSIFFPPSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSR 175

Qy 181 SGNQSQSVTEQDSKDYSLSSLTLSKADYKHVKYACVETHQGLSSPVTKSFNRGEC 239
Db 181 QNGVLNSWTDQDSKDYSSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREK 239

Query Match 55.7%; Score 691.5; DB 11; Length 234;
Best Local Similarity 54.0%; Pred. No. 4.2e-57;
Matches 129; Conservative 44; Mismatches 61; Indels 5; Gaps 1;

Qy 1 MSLPAQLGLLLLCVPGSSGEVVMVTPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MSVPTQVLGLLLCLTGARCDIQLTSPASLSASVGETVITCRASENIY-----SYLAW 55

Qy 61 YQKPGQPRLIIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEADGVYFCQGTTRP 120
Db 56 YQKQKSPQLLYVNAKTLADGVPSRFGSRGTQSLKINSIQPEDFGSYQCQHSZIP 115

Qy 121 PTFGGGKVEIKRTVAAPSVFIPPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQ 180
Db 116 FTFGSGTKLEIKRADAAPTVSIFFPPSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSR 175

Qy 181 SGNQSQSVTEQDSKDYSLSSLTLSKADYKHVKYACVETHQGLSSPVTKSFNRGEC 239
Db 181 QNGVLNSWTDQDSKDYSSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREK 234

RESULT 6
Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; IG; 2.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 55.0%; Score 682.5; DB 11; Length 234;
Best Local Similarity 55.2%; Pred. No. 3e-56;
Matches 132; Conservative 35; Mismatches 67; Indels 5; Gaps 1;

Qy 1 MSLPAQLGLLLLCVPGSSGEVVMVTPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MMSSAQFLGLLLLCFQGTTRCDIQMTQTSSLSASLGLDRVTISCRASQDISN-----YLNW 55

Qy 61 YQKPGQPRLIIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEADGVYFCQGTTRP 120
Db 56 YQKPGDGTVKLLIYTSRLYLGVPSPRFGSGSGTDSLITSNLEQEDIATYFCQGTTPP 115

Qy 121 PTFGGGKVEIKRTVAAPSVFIPPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQ 180
Db 116 FTFGSGTKLEIKRADAAPTVSIFFPPSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSR 175

Qy 181 SGNQSQSVTEQDSKDYSLSSLTLSKADYKHVKYACVETHQGLSSPVTKSFNRGEC 239
Db 176 QNGVLNSWTDQDSKDYSSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREK 234

RESULT 7
Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 53.9%; Score 669.5; DB 11; Length 234;
Best Local Similarity 54.4%; Pred. No. 5e-55;
Matches 130; Conservative 38; Mismatches 66; Indels 5; Gaps 1;

Qy 1 MSLPAQLGLLLLCVPGSSGEVVMVTPGEPASISCRSSQSLKHSNGDTFLSW 60
Db 1 MMSSAQFLGLLLLCFQGTTRCDIQMTQTSSLSASLGLDRVTISCRASQDISN-----YLNW 55

Qy 61 YQKPGQPRLIIYKVSNRDGVDPDRFSGSGAGTDFTLKISAVEADGVYFCQGTTRP 120
Db 56 YQKPGDGTVKLLIYTSRLYLGVPSPRFGSGSGTDSLITSNLEQEDIATYFCQGTTPP 115

Qy 121 PTFGGGKVEIKRTVAAPSVFIPPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQ 180
Db 116 FTFGSGTKLEIKRADAAPTVSIFFPPSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSR 175
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Db 181 SGNQSESVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
RESULT 2
Q8VC16 PRELIMINARY; PRT; 238 AA.
AC Q8VC16;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=COLON;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 69.6%; Score 864.5; DB 11; Length 238;
Best Local Similarity 68.2%; Pred. No. 2.2e-73;
Matches 163; Conservative 30; Mismatches 45; Indels 1; Gaps 1;

QY 1 MSIPQAQLGLLLCVPGSGSEVVMVTQSLPITPGEPAISICRSSQSLKHSNGDTFLSW 60
Db 1 MKLPVRL--VLMFWIPASSSDVMTQTPLSLPVLGDQASISCRSSQSLVHSNGNTYLEW 59

QY 61 YQKPGQPPRLIIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGVPFCGGQTRTP 120
Db 60 YLQKPGQSPKLLIYKVSNRFGVDPDRFSGSGGTDFTLKISRVEADLGVYFCSTHVP 119

QY 121 PTFGGKTVEIKETVAAPSVFIPPPSDEQLKSGTASVCLANNFYPREAKVQWKVDNALQ 180
Db 120 PTFGGKTLEIKRADAAPTVSIIPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSR 179

QY 181 SGNQSESVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 180 QNGVLNSWTDQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRNEC 238

Query Match 69.6%; Score 864.5; DB 11; Length 238;
Best Local Similarity 68.2%; Pred. No. 2.2e-73;
Matches 163; Conservative 30; Mismatches 45; Indels 1; Gaps 1;

QY 1 MSIPQAQLGLLLCVPGSGSEVVMVTQSLPITPGEPAISICRSSQSLKHSNGDTFLSW 60
Db 1 MKLPVRL--VLMFWIPASSSDVMTQTPLSLPVLGDQASISCRSSQSLVHSNGNTYLEW 59

QY 61 YQKPGQPPRLIIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGVPFCGGQTRTP 120
Db 60 YLQKPGQSPKLLIYKVSNRFGVDPDRFSGSGGTDFTLKISRVEADLGVYFCSTHVP 119

QY 121 PTFGGKTVEIKETVAAPSVFIPPPSDEQLKSGTASVCLANNFYPREAKVQWKVDNALQ 180
Db 120 PTFGGKTLEIKRADAAPTVSIIPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSR 179

QY 181 SGNQSESVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 180 QNGVLNSWTDQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRNEC 238

RESULT 3
Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020335; AAH02035.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003599; Ig.
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DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 67.9%; Score 843.5; DB 11; Length 238;
Best Local Similarity 66.5%; Pred. No. 2.1e-71;
Matches 159; Conservative 33; Mismatches 46; Indels 1; Gaps 1;

QY 1 MSIPQAQLGLLLCVPGSGSEVVMVTQSLPITPGEPAISICRSSQSLKHSNGDTFLSW 60
Db 1 MKLPVRL--VLMFWIPASSSDVMTQTPLSLPVLGDQASISCRSSQSLVHSNGNTYLEW 59

QY 61 YQKPGQPPRLIIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGVPFCGGQTRTP 120
Db 60 YLQKPGQSPKLLIYKVSNRFGVDPDRFSGSGGTDFTLKISRVEADLGVYFCQSHVP 119

QY 121 PTFGGKTVEIKETVAAPSVFIPPPSDEQLKSGTASVCLANNFYPREAKVQWKVDNALQ 180
Db 120 YTFGSGTKLEIKRADAAPTVSIIPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSR 179

QY 181 SGNQSESVTEQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239
Db 180 QNGVLNSWTDQDSKDYSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRNEC 238

RESULT 4
Q8VC55 PRELIMINARY; PRT; 239 AA.
AC Q8VC55;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=COLON;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021781; AAH21781.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 65.1%; Score 808; DB 11; Length 239;
Best Local Similarity 64.4%; Pred. No. 4.7e-68;
Matches 154; Conservative 32; Mismatches 53; Indels 0; Gaps 0;

QY 1 MSIPQAQLGLLLCVPGSGSEVVMVTQSLPITPGEPAISICRSSQSLKHSNGDTFLSW 60
Db 1 MKLPVLLVLLLEFTSPASSSDVLTQTPLSLPVNIGDQASISCKSLNSDGFYLDW 60

QY 61 YQKPGQPPRLIIYKVSNRDVGVPDRFSGSGAGTDFTLKISAVEADVGVPFCGGQTRTP 120
```

GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 21.6765 Seconds

(without alignments)  
2271.829 Million cell updates/sec

Title: US-09-758-173-6

Perfect score: 1242

Sequence: 1 MSLPAQLGLLLLCVPGSSG.....EVTHQGLSSPTKSFNRGEC 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1103	88.8	239	4 Q8TCD0	Q8TCD0 homo sapien
2	864.5	69.6	238	11 Q8VC16	Q8VC16 mus musculus
3	843.5	67.9	238	11 Q9NM37	Q9NM37 mus musculus
4	808	65.1	239	11 Q8VC55	Q8VC55 mus musculus
5	691.5	55.7	234	11 Q8VCP0	Q8VCP0 mus musculus
6	682.5	55.0	234	11 Q91WF8	Q91WF8 mus musculus
7	669.5	53.9	234	11 Q8R062	Q8R062 mus musculus
8	667	53.7	235	11 Q91W12	Q91W12 mus musculus
9	656.5	52.9	234	11 Q8R028	Q8R028 mus musculus
10	655.5	52.8	233	11 Q91W59	Q91W59 mus musculus
11	638.5	51.4	214	11 Q91A5	Q91A5 mus musculus
12	462.5	37.2	114	4 Q9UL80	Q9UL80 homo sapien
13	460.5	37.1	233	4 Q8TBC9	Q8TBC9 homo sapien
14	437.5	35.2	237	4 Q8WTU6	Q8WTU6 homo sapien
15	434.5	35.0	237	4 Q8WUK4	Q8WUK4 homo sapien
16	427	34.4	104	11 Q9JL82	Q9JL82 mus musculus

17	408	32.9	236	4 Q96561	Q96561 homo sapien
18	380	30.6	235	11 Q99M11	Q99M11 mus musculus
19	379.5	30.6	233	4 Q96169	Q96169 homo sapien
20	375	30.2	109	4 Q9UL78	Q9UL78 homo sapien
21	362.5	29.2	240	4 Q8WUK3	Q8WUK3 homo sapien
22	353.5	28.5	111	11 Q920E9	Q920E9 mus musculus
23	350	28.2	109	4 Q9UL85	Q9UL85 homo sapien
24	342.5	27.6	108	4 Q9UL83	Q9UL83 homo sapien
25	342	27.5	109	4 Q9UL86	Q9UL86 homo sapien
26	333.5	26.9	107	11 Q9ERZ9	Q9ERZ9 mus musculus
27	329.5	26.5	103	11 Q9JL80	Q9JL80 mus musculus
28	329.5	26.5	108	4 Q9UL79	Q9UL79 homo sapien
29	326	26.2	134	11 Q8VDD0	Q8VDD0 mus musculus
30	324	26.1	107	4 Q96SA9	Q96SA9 homo sapien
31	322.5	26.0	108	4 Q9UL77	Q9UL77 homo sapien
32	314.5	25.3	108	4 Q9UL70	Q9UL70 homo sapien
33	312.5	25.2	99	11 Q9JL74	Q9JL74 mus musculus
34	309.5	24.9	298	11 Q9QYF0	Q9QYF0 mus musculus
35	309	24.9	107	4 Q9UL81	Q9UL81 homo sapien
36	306.5	24.7	108	11 Q8VIJ0	Q8VIJ0 mus musculus
37	306.5	24.7	127	11 Q925S9	Q925S9 mus musculus
38	299.5	24.1	116	4 Q96PF6	Q96PF6 homo sapien
39	297.5	24.0	109	11 Q920E6	Q920E6 mus musculus
40	293	23.6	106	5 Q9U410	Q9U410 schistosoma
41	289.5	23.3	101	11 Q9JL78	Q9JL78 mus musculus
42	286.5	21.5	109	6 Q9N0W5	Q9N0W5 oryctolagus
43	285.5	21.4	97	11 Q9JL76	Q9JL76 mus musculus
44	260.5	21.0	107	11 Q9JL84	Q9JL84 mus musculus
45	238	19.2	241	11 Q921A6	Q921A6 mus musculus

ALIGNMENTS

RESULT 1

Q8TCD0	PRELIMINARY;	PRT;	239 AA.
ID	Q8TCD0		
AC	Q8TCD0;		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	Hypothetical 26.2 kDa protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LUNG;		
RA	Strausberg R.;		
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC023362; AAH22362.1; -		
KW	Hypothetical protein.		
SQ	SEQUENCE 239 AA; 26234 MW; FACEDCA3B03871D CRC64;		

Query Match	88.8%;	Score 1103;	DB 4;	Length 239;
Best Local Similarity	88.7%;	Pred. No. 7.6e-96;		
Matches 212;	Conservative 15;	Mismatches 12;	Indels 0;	Gaps 0;
Qy	1	MSLPAQLGLLLLCVPGSSGEVMTQSLPTTPGPASISCRSSQSLKXNGDTPLSW	60	
Db	1	MRLPAQLGLLMLVPGSSGDVMTQSLPTTPGPASISCRSTQSLVSDGNTYLNW	60	
Qy	61	YQKPGGPPRLIIYKVNRSQVDPDRFSGSGAGTDFTLKISAVEAEDGVYFCQGRTTP	120	
Db	61	FQKPGGPPRLIIYKVNRSQVDPDRFSGSGAGTDFTLKIRVEAEDGVYFCQGTHWP	120	
Qy	121	PTFGGKTKEIKRTVAAPSVEIFPPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQ	180	
Db	121	STFGGKTKEIKRTVAAPSVEIFPPSDEQLKSGTASVVCILNNFYPREAKVQKVDNALQ	180	
Qy	181	SGNSQESVTDQSDKDSYISLSTLTLSKADYKHKVYACVTHQGLSSPTKSFNRGEC	239	

Db 180 HREDYNSTLRVVSALPIQHODWMSGKEFKCKNNRSLPSPKIEKTSKRGVRAQVYVL 239  
QY 383 PPRDELTKQVSLTCLVKGFPYSDIAVWESNGQPNKYKTPPVLDSDGSFFLYSKLT 442  
Db 240 PPAEEMTKKEFSLTGMITGFLPAETAVDWTNGRTEQYKNTATVLDSDGSFYFYSKL 299  
QY 443 VDKSRVQOQNVFSCSVNHEALHNHYTKSLSPGK 478  
Db 300 VQKSTWERSLFACSVVHEVLHNHLTKTISRLGK 335

## RESULT 15

GCAM MOUSE STANDARD; PRT; 399 AA.  
AC P01865;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma-2A chain C region, membrane-bound form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8222190; PubMed=6283537;  
RA Yamawaki-kataoka Y., Nakai S., Miyata T., Honjo T.;  
RT "Nucleotide sequences of gene segments encoding membrane domains of  
immunoglobulin gamma chains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA  
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED  
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-  
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED  
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND  
SEGMENT OF MU CHAINS.  
CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE  
IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF  
THE A ALLELE.  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; J00471; AAB59661.1; ALT\_INIT.  
DR PIR; A02154; G2MSGAM.  
DR HSSP; P01842; 7FAB.  
DR MGD; MGI:96443; Igh-1.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003600; Ig\_Like.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00410; IG\_Like; 1.  
DR SMART; SM00407; IGC1; 2.  
DR PROSITE; PS00290; IG MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Transmembrane; Alternative splicing.  
FT NON\_TER 1  
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 82  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT TRANSMEM 346 363  
FT DOMAIN 364 399  
FT CARBOHYD \* 180 180  
POTENTIAL.  
CYTOPLASMIC (POTENTIAL)  
N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;  
Query Match 43.6%; Score 1117; DB 1; Length 399;  
Best Local Similarity 63.4%; Pred. No. 4e-72;  
Matches 210; Conservative 43; Mismatches 74; Indels 4; Gaps 3;  
QY 149 ASTKGPSVFLPLAPSSKTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTTTPAVLQSS 208  
Db 1 AKTTAPSVYFLAPVCGDTTGGSSVTGLCLVKGYFPEPVTLTWNSGSLSSGVHTTTPAVLQSD 60  
QY 209 GLXSLSSWTVTPSSSLGTQYICNVNHNKPSNTKVDKKAEKPKCDKTHTCPP--CPAPELL 266  
Db 61 -LYTLSSSVTVTSSTWPSQSIITCNVAHPASSTKVDDKIEPRG-PTIKPCPCCKCPAPNLL 118  
QY 267 GGPSVFLPPPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 326  
Db 119 GGPSVFIFPPPKIKDVLMLISLSPITCVVDVSDDDPDQVQISWFWNNVVEVHTAQTQTHRED 178  
QY 327 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYVTLPPSR 386  
Db 179 YNSTLRVVSALPIQHODWMSGKEFKCKVNNKDLPAPIERTISKPKGSRVAPQVYVILPPE 238  
QY 387 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKS 446  
Db 239 EEMTKQVTLTCVTDPMPEDIYVENTNNKGTLELNYKNTEPVLDSGDSFYFYSKLAVEKK 298  
QY 447 RWQGNVFSVSMHEALHNHYTKSLSPG 477  
Db 299 NWVERNSYSCSVVHEGLHNHHTTKSFRTPG 329

Search completed: March 29, 2003, 09:11:15  
Job time : 12.3969 secs



Db 1 AKTTPSVYELAPCSAAQTNSMTLGLVKGYFPPEVTVTWNSGLSSGVHTTPAVLQSD 60  
 Qy 209 GLYSLSSVTVPSSSLGITQYICNVNHPKSTKVDKKAEPKSCDKHTCP--CPAPPELL 266  
 Db 61 -LITLSSVTVPSPPSSTVTCNVNAHPASSTKVDKIVPRDCG---CKPCICTVPEV- 114  
 Qy 267 GGSFVLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 326  
 Db 115 --SSVFIFPKPKDVLITLTPKVTGVVDISKDPPEVQFSFVDDVEVHTAQTPREEQ 172  
 Qy 327 YNSTYRVSVTLTVLHODWLNKGEYKCVSNKALPAPIEKTISKAKGPRPOVYVTPPSR 386  
 Db 173 FNTSFVSELPMHODWLNKGEYKCVSNKALPAPIEKTISKAKGPRPOVYVTPPSR 232  
 Qy 387 DEITKNQVSLTCLVKGYFSDIAVWESNGOPENNYKTPPVLDSGDSFFLYSKLTVDKS 446  
 Db 233 EQMAKDKVSLTCLMIDFFPEDITVWQWNGQPAENYKNTQPMINTNGSYFVSKLVNQS 292  
 Qy 447 RMOOGNVFSCVMHEALHNNHYTKSLSPG 477  
 Db 293 NWEAGNTFTCSVLHEGLHNNHTKSLSPG 323

RESULT 12  
 GC3M\_MOUSE STANDARD; PRT; 398 AA.  
 ID GC3M\_MOUSE STANDARD; PRT; 398 AA.  
 AC P03987;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma-3 chain C region, membrane-bound form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85027161; PubMed=6092053;  
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,  
 RA Tucker P.W., Blattner F.R.;  
 RT "Structural analysis of the murine IgG3 constant region gene.";  
 RL EMBO J. 3:2041-2046(1984).  
 RN [2]  
 RP SEQUENCE OF 328-398 FROM N.A.  
 RX MEDLINE=84041483; PubMed=6314258;  
 RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,  
 RA Wall R.;  
 RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene  
 RT segment.";  
 RL Nucleic Acids Res. 11:6775-6785(1983).  
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 CC -----  
 DR EMBL; J00451; AAB59655.1; -  
 DR EMBL; V01526; CAA24767.1; ALT\_SEQ.  
 DR PIR; A02155; G3MSM.  
 DR HSSP; P01857; 1FC1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_C1.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; Ig\_Like; 1.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Transmembrane; Alternative splicing.  
 FT NON\_TER \* 1 1

FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 223 CH2.  
 FT TRANSMEM 224 327 CH3.  
 FT DOMAIN 326 362 POTENTIAL.  
 FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).  
 FT CONFLICT 333 333 E -> G (IN REF. 2).  
 FT CONFLICT 342 342 E -> Q (IN REF. 2).  
 FT CONFLICT 388 388 P -> F (IN REF. 2).  
 SQ SEQUENCE 398 AA; 43929 MW; CF7F264850A41B95 CRC64;  
 Query Match 44.0%; Score 1126; DB 1; Length 398;  
 Best Local Similarity 63.8%; Pred. No. 9.1e-73;  
 Matches 210; Conservative 46; Mismatches 69; Indels 4; Gaps 3;  
 Qy 150 STKGPSVFLPSPSKSTSGTAAALCLVKVDYFPEPTVSNWNGALTSQVHTFPAVLQSSG 209  
 Db 1 TTPAPSVFLPFGCSDTSSSVTLGLVKGYFPPEPTVKNWYNGALSSGVRTVSSVLO-SG 59  
 Qy 210 LYSLSVTVPSSSLGITQYICNVNHPKSTKVDKKAEPKSCDKHTCP--PCPAPPELLG 267  
 Db 60 FYSLSLVTVPSSTWPSQTVICNVAHPASKTELKRIEPR-IPKPSPTPPGSSCPGNIILG 118  
 Qy 268 GPSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 327  
 Db 119 GPSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 178  
 Qy 328 NSTYRVSVTLTVLHODWLNKGEYKCVSNKALPAPIEKTISKAKGPRPOVYVTPPSR 387  
 Db 179 NSTYRVSVTLTVLHODWLNKGEYKCVSNKALPAPIEKTISKAKGPRPOVYVTPPSR 238  
 Qy 388 ELTKNQVSLTCLVKGYFSDIAVWESNGOPENNYKTPPVLDSGDSFFLYSKLTVDKSR 447  
 Db 239 QMCKKVSLSLTCLVTFPFSALVWERNGELEQDYKNTPTPLDSGDTGTFYLSKLTVDTS 298  
 Qy 448 WQOGNVFSCVMHEALHNNHYTKSLSP 476  
 Db 299 WQOGNVFSCVMHEALHNNHYTKSLSP 327

RESULT 13  
 GCAA\_MOUSE STANDARD; PRT; 330 AA.  
 ID GCAA\_MOUSE STANDARD; PRT; 330 AA.  
 AC P01863;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Ig gamma-2A chain C region, A allele.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81076554; PubMed=6777755;  
 RA Sikorav J.-L., Auffray C., Rougeon F.;  
 RT "Structure of the constant and 3' untranslated regions of the murine  
 RT Balb/c gamma 2a heavy chain messenger RNA.";  
 RL Nucleic Acids Res. 8:3143-3155(1980).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81198976; PubMed=6262729;  
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;  
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene  
 RT and evolution of heavy chain genes: further evidence for intervening  
 RT sequence-mediated domain transfer.";  
 RL Nucleic Acids Res. 9:1365-1381(1981).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81223894; PubMed=6787604;  
 RA Ollio R., Auffray C., Morchamps C., Rougeon F.;  
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes  
 RT suggests that exons can be exchanged between genes in a multigenic

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CC -----  
 CC EMBL: J00451; -; NOT\_ANNOTATED\_CDS.  
 CC PIR: B02156; GIMSC.

DR HSP; P01857; IFCL.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003597; Ig\_C1.

DR InterPro; IPR003600; Ig\_Like.

DR Pfam; PF00047; Ig\_3.

DR SMART; SM00410; Ig\_Like; 1.

DR SMART; SM00407; IGCL; 2.

DR PROSITE; PS00290; Ig\_MHC; 1.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW Transmembrane; Alternative splicing.

FT NON TER 1 1

FT DOMAIN 1 97

FT CH1.

FT DOMAIN 98 113

FT HINGE.

FT DOMAIN 114 223

FT CH2.

FT DOMAIN 224 327

FT CH3.

SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 44.4%; Score 1137; DB 1; Length 329;

Best Local Similarity 64.0%; Pred. No. 1.2e-73;

Matches 212; Conservative 46; Mismatches 69; Indels 4; Gaps 3;

Qy 150 STKGPSVFPLAPSKSGTGAALGLVDFPEPVTVSWNSGALTVGVHTFPVAVLQSSG 209

Db 1 TTTAPSVYPLPGCSGTSSTSSVTLGLVKGYPFVPTVKNVYALSSGVRVTVSLQ-SG 59

Qy 210 LYLSSVTVVPSLSGTQYICNVNHPKNTKDKKAPKSCDKTHTCP--PCPAPELLG 267

Db 60 FYSLSLVTVPSSTWPSQTVICNVAHPASKTELKRIEPR-IPKSTPFGSGSCPFGNIGL 118

Qy 268 GPSVFLFPKPKDTLMSPTPEVTCVVVDVSHEDPEVENYVDGVENVNAKTPREQY 327

Db 119 GPSVFLFPKPKDLMISLTPKVTCTVVDVSDPDVHVSFVMDKVEVHTAWTPQRAQY 178

Qy 328 NSTYRVVSVLTVLQDWLNGKEYCKVKVSKALPAPIETISKAKGQPREPOVYTLPPSRD 387

Db 179 NSTFRVVSALPIQHDDMRGKEFKCKVKNKALPAPIETISKAKGQRAQTPQVYTIPTPRE 238

Qy 388 ELTKNQLVSLCLVKGYPFSDIAVEHNSGQPENNYKTPPVLDSGSPFLYSKLTVDKSR 447

Db 239 QMSKKVSLTCLVTNPFSAISVEMERNGELEQDYKNTPPILDSGTYFLYSKLTVDKSR 298

Qy 448 WQGNVFCVSMHEALHNYTKQSLSPGK 478

Db 299 WLQGEIFTCVSVHVALHNNHTQKLSRSPGK 329

RESULT 11

ID GC1M MOUSE STANDARD; PRT; 393 AA.

AC P01869;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Ig gamma-1 chain C region, membrane-bound form.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=80045036; PubMed=115593;

RA Honjo T., Obara M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,

RA Takahashi N., Mano Y.;

RT "Cloning and complete nucleotide sequence of mouse immunoglobulin

gamma 1 chain gene.;"

RL Cell 18:559-568(1979).

RN [2]

RP SEQUENCE OF 323-393 FROM N.A.  
 RX MEDLINE=82197626; PubMed=6804950;  
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;

RT "mRNA for surface immunoglobulin gamma chains encodes a highly

conserved transmembrane sequence and a 28-residue intracellular

domain.;"

RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).

RN [3]

RP SEQUENCE OF 323-366 FROM N.A.

RX MEDLINE=82115295; PubMed=6799207;

RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,

RA Eisenberg D., Wall R.;

RT "Gene segments encoding transmembrane carboxyl termini of

immunoglobulin gamma chains.;"

RL Cell 26:19-27(1981).

RN [4]

RP SEQUENCE OF 1-44 FROM N.A.

RX MEDLINE=8222190; PubMed=6283537;

RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;

RT "Nucleotide sequences of gene segments encoding membrane domains of

immunoglobulin gamma chains.;"

RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA

SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED

GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-

BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED

IN SEPARATE EXONS. THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND

SEGMENT OF MU CHAINS.

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CC EMBL; V00793; CAA24172.1; -.

DR EMBL; V00793; CAA24173.1; -.

DR EMBL; V00793; CAA24174.1; -.

DR PIR; B02159; GIMSM.

DR HSSP; P01842; 7FAB.

DR MGD; MGI:96446; Igh-4.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003597; Ig\_C1.

DR Pfam; PF00047; Ig\_3.

DR SMART; SM00407; IGCL; 2.

DR PROSITE; PS00290; Ig\_MHC; 1.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW Alternative splicing; Transmembrane.

FT NON TER 1 1

FT DOMAIN 1 97

FT CH1.

FT HINGE.

FT DOMAIN 98 110

FT CH2.

FT DOMAIN 111 217

FT CH3.

FT DOMAIN 218 324

FT DISULFID 27 82

FT DISULFID 102 102

FT DISULFID 104 104

FT DISULFID 107 107

FT DISULFID 109 109

FT DISULFID 138 198

FT DISULFID 174 174

FT CARBOHYD 244 302

FT DISULFID 340 357

FT TRANSMEM 340 357

FT DOMAIN 358 393

SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 44.2%; Score 1133; DB 1; Length 393;

Best Local Similarity 61.9%; Pred. No. 2.9e-73;

Matches 205; Conservative 55; Mismatches 61; Indels 10; Gaps 4;

Qy 149 ASTKGPSVFPLAPSKSGTGAALGLVDFPEPVTVSWNSGALTVGVHTFPVAVLQSS 208

Db 1 TTTAPSVYPLPGCSGTSSTSSVTLGLVKGYPFVPTVKNVYALSSGVRVTVSLQ-SG 59

Qy 210 LYLSSVTVVPSLSGTQYICNVNHPKNTKDKKAPKSCDKTHTCP--PCPAPELLG 267

Db 60 FYSLSLVTVPSSTWPSQTVICNVAHPASKTELKRIEPR-IPKSTPFGSGSCPFGNIGL 118

Qy 268 GPSVFLFPKPKDTLMSPTPEVTCVVVDVSHEDPEVENYVDGVENVNAKTPREQY 327

Db 119 GPSVFLFPKPKDLMISLTPKVTCTVVDVSDPDVHVSFVMDKVEVHTAWTPQRAQY 178

Qy 328 NSTYRVVSVLTVLQDWLNGKEYCKVKVSKALPAPIETISKAKGQPREPOVYTLPPSRD 387

Db 179 NSTFRVVSALPIQHDDMRGKEFKCKVKNKALPAPIETISKAKGQRAQTPQVYTIPTPRE 238

Qy 388 ELTKNQLVSLCLVKGYPFSDIAVEHNSGQPENNYKTPPVLDSGSPFLYSKLTVDKSR 447

Db 239 QMSKKVSLTCLVTNPFSAISVEMERNGELEQDYKNTPPILDSGTYFLYSKLTVDKSR 298

Qy 448 WQGNVFCVSMHEALHNYTKQSLSPGK 478

Db 299 WLQGEIFTCVSVHVALHNNHTQKLSRSPGK 329



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RESULT 9
GC1_MOUSE
AC P01868; STANDARD; PRT; 324 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adefugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
murine myeloma gamma chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulfide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
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CC -----
DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR EMBL; V00793; CAA24175.1; -
DR EMBL; V00793; CAA24176.1; -
DR PIR; A02159; G1MS.
DR HSP; P01842; 7FAB.
DR GlycoSuiteDB; P01868; --
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; immunoglobulin C region; Glycoprotein;

```

```

KW Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 98 110 CH1.
FT DOMAIN 111 217 HINGE.
FT DOMAIN 218 324 CH2.
FT DISULFID 27 82 CH3.
FT DISULFID 102 102
FT DISULFID 104 104 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198 INTERCHAIN (WITH A HEAVY CHAIN).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .).
FT DISULFID 244 302 /FTId-CAR_000055.
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match 44.4%; Score 1138; DB 1; Length 324;
Best Local Similarity 62.0%; Pred. No. 9.9e-74;
Matches 206; Conservative 55; Mismatches 61; Indels 10; Gaps 4;

QY 149 ASTKGPVSFPLAPSSKSTSGCTAALGCLVKDYRPEPVTVSWNSGALTSGVHTFPAVLQSS 208
Db 1 AKTPPSVYPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 60
QY 209 GLXSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPP--CPAPELL 266
Db 61 -LYTSLSSVTPSSPRPSETVTCNVAHPASSTKVDKVIKPRDCG----CKPFCITVPEV- 114
QY 267 GGSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQ 326
Db 115 --SSVFIFPPKPKDVLITLTTPKTCVVVDISKDDPEQVSWFVDDVEVHTAQTQPREEQ 172
QY 327 YNSTYRVSVLTVLHODWLNKGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYITLPPSR 386
Db 173 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEKTIKTKGRKPAQVYITLPPPK 232
QY 387 DELTKQVSTLCVLKGYFPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKS 446
Db 233 EQMAKDKVSLTCTMTDFFPEDITVEWQWNGQPAENYKNTQPIINTNGSVFVYSKLVNQS 292
QY 447 RWOQGNVFCSCVMHEALHNHYTOKSLSLSPGK 478
Db 293 NWEAGNTFTCSVLHEGLHHHTKSLSHSPGK 324

RESULT 10
GC3_MOUSE
ID GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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QY 373 QPREQVYTLPSRDELTKNOVSLCLVKGFYPSDIAVWESNGOPENNYKTPPVLDS 432
Db 185 QPREQVYTLPSREBEMTKNOVSLCLVKGFYPSDIAVWESSGOPENNYKTPPMLDS 244
QY 433 GSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 478
Db 245 GSFFLYSKLTVDKSRWQGNIFCSCVMHEALHNHYTKQSLSPGK 290

RESULT 7
GCL_RAT ID_GCL_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 44.8%; Score 1148; DB 1; Length 326;
Best Local Similarity 63.1%; Pred. No. 2e-74;
Matches 210; Conservative 52; Mismatches 61; Indels 10; Gaps 4;

QY 149 ASTKGPSVFLPAPSSKSTSGGTAALCLVKDYFPPVTVSWNSGALTSGVHTFPAVLQSS 208
Db 1 AETAPSVYPLAPGALKNSVMVTLGCLVKGYFPPVTVTWSNGALSSGVHTFPAVLQ-S 59
QY 209 GLYSLSSVTVTPSSSLGTOTYICNVNHKPSNTKVDKAEKPSKCDTHRCPPCAPPELLGG 268
Db 60 GLYTLTSSVTVTPSSVTSQVTCNVNAPASSTKVDKKVPRNCG--GDCKPC---ICTG 113
QY 269 ---PSVFLPPPKDGLMIKSRPEVTVVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 325
Db 114 SEVSSVFIIPPKPKDVLITLTPKVTCCVVDVDSQDDPEVHFSWFVDVEVHTAQTREE 173
QY 326 QYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKGQPREPQVYTLPS 385
Db 174 QFNSTFRSVSELPILHODWLNKGRTRCKVTSAAFPSPIEKTSKPEGRQVPHVYTNSTP 233
QY 386 RDELTKNOVSLCLVKGFYPSDIAVWESNGOPENNYKTPPVLDSGGSFFLYSKLTVDK 445
Db 234 KEEMTQNEVITCMVKWGFPPDIYVEWQNGQPQENYKNTPTPTMDTDSGYFLYSLKLVKK 293
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QY 446 SRWQGNVFCSCVMHEALHNHYTKQSLSPGK 478
Db 294 ERWQGNFTCTSVLHGLHNHHTKSLSPGK 326

RESULT 8
GCB_RAT ID_GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
FT SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 44.6%; Score 1142.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 4.9e-74;
Matches 214; Conservative 44; Mismatches 69; Indels 9; Gaps 3;

QY 149 ASTKGPSVFLPAPSSKSTSGGTAALCLVKDYFPPVTVSWNSGALTSGVHTFPAVLQSS 208
Db 1 AQTAPSVYPLAPGCGDTSSTVTGLCLVKGYFPPVTVTWSNGALSSDVHTFPAVLQ-S 59
QY 209 GLYSLSSVTVTPSSSLGTOTYICNVNHKPSNTKVDKAEKPSK-----CDKHTCPCPA 262
Db 60 GLYTLTSSVTVTPSSVTSQVTCNVNAPASSTKVDKKVRRNGIGHKCPTCTCHKCPV 117
QY 263 PELIGSPSVFLPPPKPKDGLMIKSRPEVTVVVDVSHEDPEVKFNWYDGVGVHNAKTP 322
Db 118 PELIGSPSVFIIPPKPKDILLISQNAKVTICVVVDVSEEPDQVFSFVNNVEVHTAQTQ 177
QY 323 REQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKGQPREPQVYTL 382
Db 178 REQYNSTFRVSWALPIHQDWMNSGKEFKCKVNNKALPSPIEKTSKPKGLVKRPQVYVM 237
QY 383 PPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTPPVLDSGGSFFLYSKLT 442
Db 238 GPPTQTEQTEQVTLTCLTSLTSGFLPNDIGVWTSNGHLEKNKNTPEPVDSDGGSFFMYSKLN 297
QY 443 VDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 478
Db 298 VERSRWDSRAPFVCSVVHGLHNHHEKSISSRPFGK 333
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DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 V -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 47.9%; Score 1226.5; DB 1; Length 323;
Best Local Similarity 69.7%; Pred. No. 5.2e-80;
Matches 228; Conservative 34; Mismatches 58; Indels 7; Gaps 2;

QY 152 KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPVTVSWNSGALTSGVHTFPAVLQSSGLY 211
DB 4 KAPSVFPLAPCCGTPSSTVTGLGCLVKGLPEPTVWNSGTLTGNGVTRTFPSVROSSGLY 63
QY 212 SLSSVTVTPSSSLGTQTYICNVNHKPSNTKVKAEKPSCKDTHTCPPCAPPELLGGPSV 271
DB 64 SLSSVTVTPSSS---QPVTCNVAHAPATNKVDKTVAPSTCSK----PTCPPPELLGGPSV 116
QY 272 FLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 331
DB 117 FLFPPKPKDTLMISRTPEVTCVVDVSDQDPEVQFTWYINNEQVTRAPPLREQQFNSTI 176
QY 332 RVVSVLTIVLHODWLNKGEYKCKVKSNKALPAPIETKTISKAKGQPREPOVYITLPSSDELTK 391
DB 177 RVVSVLTIVHODWLNKGEYKCKVKSNKALPAPIETKTISKARGQPLEPKVYITMGPPREELSS 236
QY 392 NOVSLTCLVKGFPPSDIAVEWESNGOPENNYKTTTPVLDSDGSFELYSKLTVDKSRWQQG 451
DB 237 RVSVLTCTMGNGYPPSDISVEWENKGAEDNYKTTTAVLDSDGSFLYKNKLSVPTSEWQRG 296
QY 452 NVFSCSVMEALHNHYTQKSLSLSPGK 478
DB 297 DVFTCSVMHEALHNHYTQKSISRSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Biraghtein B.K.; Hussein Q.Z.; Cebra J.J.;
```

```
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J.; Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E.; Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M.; Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B.; Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1PBA9 CRC64;

Query Match 47.3%; Score 1212.5; DB 1; Length 329;
Best Local Similarity 70.1%; Pred. No. 5.3e-79;
Matches 234; Conservative 28; Mismatches 63; Indels 9; Gaps 4;

QY 148 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPVTVSWNSGALTSGVHTFPAVLQ 207
DB 1 SARTAPSFVPLAASCVDTSQSMWTLGCLVKGYFPPVTVKWSGALTSGVHTFPAVLQ- 59
QY 208 SGLYSLSVVTVTPSSSLGTQTYICNVNHKPSNTKVKAEKPSCKDTH--TCPCCPAPEL 265
DB 60 SGLYSLSVTMTVPSSQKAT----CNVAHPASSTKVDTVEPIPTPZBPBCTCKCPPEP 115
QY 266 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 325
DB 116 LGGPSVFIFFPKPKDTLMISLTTPRVTCVVDVSDQDPEVQFTWFDNKPVGNAETKPRVE 175
QY 326 QYNSTYRVSVLTIVLHODWLNKGEYKCKVKSNKALPAPIETKTISKAKGQPREPOVYITLPPS 385
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DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig gamma-4 chain C region.  
 GN IGHG4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83157104; PubMed=6299862;  
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;  
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";  
 RL DNA 1:11-18(1981).  
 RN [2]  
 RP SEQUENCE OF 1-30 AND 81-326.  
 RX MEDLINE=70207560; PubMed=4192699;  
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;  
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the  
 constant region of a gamma 4 chain.";  
 RL Biochem. J. 117:33-47(1970).  
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 CC -----  
 DR EMBL; K01316; AAB59394.1; ALT\_INIT.  
 DR PIR; A02150; G4HU.  
 DR HSP; P01842; 7FAB.  
 DR Genew; HGNC:5528; IGHG4.  
 DR MIM; 147130; .  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003597; Ig C1.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; Ig like; 1.  
 DR SMART; SM00407; IGH1; 2.  
 DR PROSITE; PS00290; Ig MHC; 2.  
 DR Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 1  
 FT CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 220 CH2.  
 FT DOMAIN 221 327 CH3.  
 FT INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 14 14  
 FT DISULFID 27 83  
 FT INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106  
 FT DISULFID 109 109  
 FT DISULFID 141 201  
 FT DISULFID 247 305  
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811BF208E7A CRC64;  
  
 Query Match 61.9%; Score 1586.5; DB 1; Length 327;  
 Best Local Similarity 90.6%; Pred No. 1.6e-105;  
 Matches 299; Conservative 12; Mismatches 16; Indels 3; Gaps 1;  
  
 QY 149 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 208  
 Db 1 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60  
  
 QY 209 GLYSLSSVTVPSSTIGTQTYICNVNPKSNITKVDKAPKSCDKTHCTCPCPAPRLGG 268  
 Db GLYSLSSVTVPSSTIGTQTYICNVNPKSNITKVDKRVESK---YCPCPSCPAPRLGG 117  
  
 QY 269 PSVFLPPPKKOTLMISRPETVCVVVDVSHEDPEVKENWYVDGVEVNAKTKPREQYN 328  
 Db PSVFLPPPKKOTLMISRPETVCVVVDVSHEDPEVKENWYVDGVEVNAKTKPREQYN 177  
  
 QY 329 STYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQRPQVYTLPPSQSE 388  
 Db STYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQRPQVYTLPPSQSE 237

Db 178 STYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQRPQVYTLPPSQSE 237  
 QY 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYYKSLTVDKSRW 448  
 Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFYYKSLTVDKSRW 297  
 QY 449 QCGNVFSCSVMEALHNYHTOKSLSPGK 478  
 Db 298 QCGNVFSCSVMEALHNYHTOKSLSPGK 327  
  
 RESULT 4  
 GC\_RABIT  
 ID GC\_RABIT STANDARD; PRT; 323 AA.  
 AC F01870;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma chain C region.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84030930; PubMed=6313520;  
 RA Bernstein K.E., Alexander C.B., Mage R.G.;  
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant  
 F-1 haplotype.";  
 RL Immunogenetics 18:387-397(1983).  
 RN [2]  
 RP SEQUENCE OF 1-128.  
 RX MEDLINE=76135469; PubMed=1243651;  
 RA Pratt D.M., Mole L.E.;  
 RT "Sequence studies on the constant region of the Fd sections of rabbit  
 immunoglobulin G of different allotype.";  
 RL Biochem. J. 151:337-349(1975).  
 RN [3]  
 RP SEQUENCE OF 88-266 FROM N.A.  
 RX MEDLINE=83299917; PubMed=6193512;  
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma  
 heavy chain and identification of two genomic C gamma genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
 RN [4]  
 RP SEQUENCE OF 132-161.  
 RX MEDLINE=70110015; PubMed=5461106;  
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
 RT "Sequence studies of the Fd section of the heavy chain of rabbit  
 immunoglobulin G";  
 RL Biochem. J. 116:249-259(1970).  
 RN [5]  
 RP SEQUENCE OF 129-131 AND 155-322.  
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
 RL (In) Kiliander J. (eds.);  
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
 RL Stockholm (1967).  
 CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,  
 CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15  
 CC MARKERS AND REF.5 THE E15 MARKER.  
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 CC -----  
 DR EMBL; M16426; AAA31289.1; .  
 DR PIR; A02161; GHRB.  
 DR HSP; P01857; 1FC1.  
 DR InterPro; IPR003006; Ig\_MHC.

OX NCBI:TaxID=9606;  
RN [1]  
RP SEQUENCE OF 2-326 FROM N.A.  
RX MEDLINE=82197621; PubMed=6804948;  
RA Ellison J.W., Hood L.E.;  
RT "Linkage and sequence homology of two human immunoglobulin gamma  
RT heavy chain constant region genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
RN [2]  
RP SEQUENCE OF 88-115 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=83001943; PubMed=6811139;  
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;  
RT "Structure of human immunoglobulin gamma genes: implications for  
RT evolution of a gene family.";  
RL Cell 29:671-679(1982).  
RN [3]  
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=84235992; PubMed=6329676;  
RA Krawinkel U., Rabbitts T.H.;  
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
RT genes.";  
RL EMBO J. 1:403-407(1982).  
RN [4]  
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
RX MEDLINE=81007873; PubMed=6774012;  
RA Wang A.-C., Tung E., Fudenberg H.H.;  
RT "The primary structure of a human IgG2 heavy chain: genetic,  
RT evolutionary, and functional implications.";  
RL J. Immunol. 125:1048-1054(1980).  
RN [5]  
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
RX MEDLINE=8001357; PubMed=113060;  
RA Connell G.E., Parr D.M., Hofmann T.;  
RT "The amino acid sequences of the three heavy chain constant region  
RT domains of a human IgG2 myeloma protein.";  
RL Can. J. Biochem. 57:758-767(1979).  
RN [6]  
RP SEQUENCE OF 238-275 (ZIE).  
RX MEDLINE=80114419; PubMed=118920;  
RA Hofmann T., Parr D.M.;  
RT "A note of the amino acid sequence of residues 381-391 of human  
RT immunoglobulin gamma chains.";  
RL Mol. Immunol. 16:923-925(1979).  
RN [7]  
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
RA Hofmann T., Parr D.M.;  
RL Submitted (MAR-1980) to the PIR data bank.  
RN [8]  
RP SEQUENCE OF 1-121 (DOT).  
RX MEDLINE=95255298; PubMed=7737190;  
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
RT "Characterization of the two unique human anti-flavin monoclonal  
RT immunoglobulins.";  
RL Eur. J. Biochem. 228:886-893(1995).  
RN [9]  
RP DISULFIDE BONDS.  
RX MEDLINE=72033500; PubMed=4940472;  
RA Milstein C., Frangione B.;  
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";  
RL Biochem. J. 121:217-225(1971).  
RN [10]  
RP DISULFIDE BONDS.  
RX MEDLINE=69064124; PubMed=5782707;  
RA Frangione B., Milstein C., Pink J.R.L.;  
RT "Structural studies of immunoglobulin G.";  
RL Nature 221:145-148(1969).  
RN [11]  
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CC -----  
DR EMBL: J00230; AAB59393.1; -.  
DR PIR: A02148; G2HU.  
DR HSP: P01857; 1FC1.  
DR Genew: HGNC:5526; IGHG2.  
DR MIM: 147110; -.  
DR InterPro: IPR003006; Ig MHC.  
DR InterPro: IPR003597; Ig cl.  
DR InterPro: IPR003600; Ig\_like.  
DR Pfam: PF00047; ig; 3.  
DR SMART: SM00410; Ig\_like; 1.  
DR SMART: SM00407; IGH1; 2.  
DR PROSITE: PS00290; Ig MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 219 CH2.  
FT DOMAIN 220 326 CH3.  
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 83  
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
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FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;  
SQ  
Query Match 62.5%; Score 1600; DB 1; Length 326;  
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Matches 300; Conservative 12; Mismatches 14; Indels 4; Gaps 2;  
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DB 61 GLYSLSSVTVPRSSSLGTQYICNVNHNKPSNTKVDKAPKSCDKHTHTCPCPAPPELLGG 116  
QY 269 PSVFLFPPPKDPTLMISRTPEVTCTVVVDVSHEDPEVKFNWYVDGVVHNKAKTPREEQYN 328  
DB 117 PSVFLFPPPKDPTLMISRTPEVTCTVVVDVSHEDPEVKFNWYVDGVVHNKAKTPREEQYN 176  
QY 329 STYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388  
DB 177 STYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 236  
QY 389 LTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFELYSLKLTVDKSRW 448  
DB 237 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFELYSLKLTVDKSRW 296  
QY 449 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 478  
DB 297 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 326  
RESULT 3  
GC4\_HUMAN STANDARD; PRT; 327 AA.  
AC P01861;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)

RT Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [7]  
RP DISULFIDE BONDS.  
RX MEDLINE=77070267; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
RT characterization of the protein, the L- and H-chains, the  
RT cyanogen bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370(1981).  
CC GIM(1) MARKERS, 239-D & 241-L, KOL & EU SEQUENCES HAVE THE GIM(3)  
CC MARKER & THE GIM (NON-1) MARKERS.  
CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF  
CC 35,116,198,269 & 272.  
CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
CC 268-272.  
CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
CC RESIDUES 198,267&272.  
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CC -----  
DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
DR PIR; A02146; GHU.  
DR PDB; 1FC1; 15-JUL-92.  
DR PDB; 1FC2; 15-JUL-92.  
DR Genew; HGNC:5525; IGHG1.  
DR MIM; 147100; -.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003600; Ig\_like.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00410; Ig like; 1.  
DR SMART; SM00407; IGHG1; 2.  
DR PROSITE; PS00290; IG MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW 3D-structure.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 223 CH2.  
FT DOMAIN 224 330 CH3.  
FT DISULFID 27 83  
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).  
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FT VARIANT 241 241 REMOVED POST-TRANSLATIONALLY.  
FT VARIANT 241 241 K -> R (IN GIM(3) MARKER).  
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FT /FTIG=VAR\_003888.  
FT /FTIG=VAR\_003889.

FT HELIX 130 134  
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FT STRAND 175 178  
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FT TURN 267 268  
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FT STRAND 274 276  
FT STRAND 280 281  
FT TURN 283 284  
FT STRAND 287 296  
FT HELIX 297 301  
FT TURN 302 303  
FT STRAND 306 312  
FT TURN 313 314  
FT TURN 316 317  
FT STRAND 320 324  
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Query Match 68.8%; Score 1763; DB 1; Length 330;  
Best Local Similarity 99.7%; Pred. No. 4.8e-118;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 149 ASTKGSVPFLAPSSKSTGGTAAALCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 208  
Db 1 ASTKGSVPFLAPSSKSTGGTAAALCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60  
QY 209 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKAKPKSCDKTHTCPPCPAPPELLGG 268  
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKAKPKSCDKTHTCPPCPAPPELLGG 120  
QY 269 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 328  
Db 121 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
QY 329 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388  
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
QY 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 448  
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
QY 449 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 478  
Db 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330  
RESULT 2  
GC2\_HUMAN  
ID GC2\_HUMAN STANDARD; PRT; 326 AA.  
AC P01859;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-2 chain C region.  
GN IGHG2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:23 ; Search time 11.3969 Seconds  
(without alignments)  
1739.566 Million cell updates/sec

Title: US-09-758-173-8

Perfect score: 2561

Sequence: 1 MWSSILLFLVAVATRVQCE.....MHEALHNHYTKSLSPGK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1763	68.8	330	1 GCI_HUMAN	P01857 homo sapien
2	1600	62.5	326	1 GCI_HUMAN	P01859 homo sapien
3	1586.5	61.9	327	1 GCI_HUMAN	P01861 homo sapien
4	1226.5	47.9	323	1 GC_RABIT	P01870 oryctolagus
5	1212.5	47.3	329	1 GCI_HUMAN	P01862 cavia porce
6	1157	45.2	320	1 GCI_HUMAN	P01860 homo sapien
7	1148	44.8	326	1 GCI_HUMAN	P01869 mus musculus
8	1142.5	44.6	333	1 GCB_RAT	P20759 rattus norv
9	1138	44.4	324	1 GCI_MOUSE	P20761 rattus norv
10	1137	44.4	329	1 GCI_MOUSE	P01868 mus musculus
11	1133	44.2	329	1 GCI_MOUSE	P22436 mus musculus
12	1126	44.0	398	1 GCI_MOUSE	P01869 mus musculus
13	1122	43.8	330	1 GCAA_MOUSE	P03987 mus musculus
14	1119.5	43.7	335	1 GCB_MOUSE	P01863 mus musculus
15	1117	43.6	399	1 GCAM_MOUSE	P01864 mus musculus
16	1114.5	43.5	329	1 GCI_MOUSE	P01865 mus musculus
17	1108	43.3	322	1 GCB_RAT	P20762 rattus norv
18	1085	42.4	336	1 GCB_MOUSE	P20760 rattus norv
19	1080	42.2	405	1 GCB_MOUSE	P01866 mus musculus
20	489	19.1	428	1 EPC_HUMAN	P01867 mus musculus
21	483.5	18.9	429	1 EPC_RAT	P01854 homo sapien
22	465	18.2	421	1 EPC_MOUSE	P01855 rattus norv
23	448	17.5	455	1 MUC_MOUSE	P06336 mus musculus
24	442	17.3	142	1 HV01_RAT	P01872 mus musculus
25	442	17.3	454	1 MUC_HUMAN	P01805 rattus norv
26	438	17.1	476	1 MUC_MOUSE	P01871 homo sapien
27	437	17.1	458	1 MUC_RABIT	P01873 mus musculus
28	430	16.8	144	1 HV26_MOUSE	P03988 oryctolagus
29	427	16.7	479	1 MUCM_RABIT	P01795 mus musculus
30	425	16.6	451	1 MUC_MOUSE	P04221 oryctolagus
31	420	16.4	450	1 MUC_CANFA	P20768 suncus muri
32	419	16.4	123	1 HV18_MOUSE	P01874 canis fami
33	418.5	16.3	122	1 HV20_MOUSE	P01787 mus musculus
					P01789 mus musculus

34	418	16.3	123	1	HV19_MOUSE	P01788 mus musculu
35	416.5	16.3	122	1	HV21_MOUSE	P01790 mus musculu
36	416	16.2	117	1	HV17_MOUSE	P01786 mus musculu
37	415.5	16.2	454	1	MUC_MESAU	P06337 mesocricetu
38	415	16.2	123	1	HV22_MOUSE	P01791 mus musculu
39	410	16.0	123	1	HV23_MOUSE	P01792 mus musculu
40	403	15.7	391	1	MUCB_HUMAN	P04220 homo sapien
41	399	15.6	123	1	HV25_MOUSE	P01794 mus musculu
42	397	15.5	117	1	HV3C_HUMAN	P01764 homo sapien
43	397	15.5	123	1	HV24_MOUSE	P01793 mus musculu
44	396	15.5	115	1	HV32_MOUSE	P01801 mus musculu
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## ALIGNMENTS

RESULT 1  
GCI\_HUMAN  
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AC P01857;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-1 chain C region.  
GN IGHG1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Berson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RA Maxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RA Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.



Db 229 STTVDKLPEPGSTINPCPPCKCKECPAPNLEGPSVFIFPNKIDVLMISLTPEKVT 288  
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 QY 352 CKVSNKALPAPIETISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVE 411  
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 QY 412 WSNQGNPNYKTPPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQS 471  
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 Db 469 ISRSPGK 475

## RESULT 14

Ig Gamma 2a chain constant region - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C:Accession: I47159  
 R:Kaczkovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994  
 A:Title: Five putative subclasses of swine IGG identified from the cDNA sequences of a s  
 A:Reference number: I47158; MUID:95015845; PMID:7930579  
 A:Accession: I47159  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-328 <KAC>  
 A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124  
 C:Genetics:  
 A:Gene: IgG2a  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 49.2%; Score 1259; DB 2; Length 328;  
 Best Local Similarity 69.3%; Pred. No. 1.8e-67;  
 Matches 230; Conservative 43; Mismatches 53; Indels 6; Gaps 2;

QY 149 ASTKGPSVPLAPSKSTSGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS 208  
 Db 1 AKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVSNWNSGALTSGVHTFPAVLQSS 60  
 QY 209 GLYSLSSVTVPSLSLTQTYICNVNHNKSNKTKVDKKAEPKSCDKTHTCPPCPAPPELLGG 268  
 Db 61 GLYSLSSMTVPASSLSKSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP---G 116  
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 Db 117 PSVFIFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 176  
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 QY 447 RWOQGNVFCSCVMHEALHNHYTKQSLSPGK 478  
 Db 297 SWQGGIFQCAVMHEALHNHYTKQSLSPGK 328

## RESULT 15

S31866  
 Ig gamma-1 chain C region - synthetic  
 C:Species: synthetic

A:Note: Homo sapiens (man) Gene engineered and expressed in Escherichia coli  
 C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
 C:Accession: S31866  
 R:Filpula, D.  
 submitted to the EMBL Data Library, February 1993  
 A:Description: Screening method for protein-protein interactions of cloned gene products.  
 A:Reference number: S31866  
 A:Accession: S31866  
 A:Molecule type: mRNA  
 A:Residues: 1-255 <FIL>  
 A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069  
 C:Keywords: immunoglobulin  
 F:1-22/Region: Escherichia coli outer membrane protein A precursor  
 F:23-255/Region: human Ig gamma-1 chain C region

Query Match 49.0%; Score 1256; DB 4; Length 255;  
 Best Local Similarity 97.1%; Pred. No. 2.1e-67;  
 Matches 232; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 240 TKVYKKAEPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSH 299  
 Db 17 TVAQADVESKCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSH 76  
 QY 300 EDEPVKFNWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKAL 359  
 Db 77 EDEPVKFNWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKAL 136  
 QY 360 PAPIETISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGQPE 419  
 Db 137 PAPIETISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGQPE 196  
 QY 420 NNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 478  
 Db 197 NNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 255

Search completed: March 29, 2003, 09:16:19  
 Job time : 22.453 secs

A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <FIS>  
 A:Cross-references: EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827  
 R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
 Nature 283, 786-789, 1980  
 A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from H  
 A:Reference number: A02157; MUID:80120716; PMID:6765534  
 A:Contents: a allele  
 A:Accession: A02157  
 A:Molecule type: DNA  
 A:Residues: 138-161, '1', 163-189, 'FP', 193-474 <YAM>  
 A:Cross-references: GB:J00461  
 A:Note: The sequence was determined from the germline gene  
 R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
 Science 206, 1299-1303, 1979  
 A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy  
 A:Reference number: A26235; MUID:80081501; PMID:117548  
 A:Contents: MPC 11  
 A:Accession: A26235  
 A:Molecule type: mRNA  
 A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>  
 A:Note: Lys-474 is probably removed posttranslationally  
 R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
 Science 206, 1303-1306, 1979  
 A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin  
 A:Reference number: A26232; MUID:80081502; PMID:117549  
 A:Accession: A26232  
 A:Molecule type: DNA  
 A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>  
 R:Ollo, R.; Rougeon, F.  
 Nature 296, 761-763, 1982  
 A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma  
 A:Reference number: A26233; MUID:82173203; PMID:6803173  
 A:Contents: b allele  
 A:Accession: A26233  
 A:Molecule type: DNA  
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLI>  
 A:Cross-references: GB:J00461  
 R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi  
 J. Biol. Chem. 269, 12345-12350, 1994  
 A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
 A:Reference number: A53598; MUID:94216359; PMID:7512967  
 A:Accession: A53598  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 234-251 <KIM>  
 A:Comment: The a allele sequence is shown.  
 C:Genetics: 138/1; 236/1; 258/1; 368/1  
 A:Antibody: 138/1; 236/1; 258/1; 368/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul  
 F:157-222/Domain: immunoglobulin homology <IMI>  
 F:236-257/Region: hinge  
 F:281-350/Domain: immunoglobulin homology <IM2>  
 F:387-454/Domain: immunoglobulin homology <IM3>  
 F:152/Disulfide bonds: interchain (to light chain) #status predicted  
 F:164-220, 288-348, 394-452/Disulfide bonds: #status predicted  
 F:247-250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted  
 F:324/Binding site: carbohydrate (asn) (covalent) #status predicted  
 Query Match 54.4%; Score 1392; DB 1; Length 474;  
 Best Local Similarity 54.6%; Pred. No. 3.8e-75;  
 Matches 265; Conservative 73; Mismatches 129; Indels 18; Gaps 4;  
 QY 1 MGWSLLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60  
 DB 1 MEWSWIFLLSGTAGVHSEVQLQSGPELVWFCASVWMSCKASGYTFYTHYHWVQKP 60  
 QY 61 GKGPEWVGFIKPNKGGTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYVCTTS 120

DB 61 QGGLWIGYI--NPNKDGTKFNEKFKGKATLTSDKSSNTAYMELSLTSDSAVYYCARD 118  
 QY 121 YISHCRGGVCYGVYFPGWQCALVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDY 180  
 DB 119 YDY-----DWFAWYGQGLTVTVSAAKTTPPSVYPLAPGCGDTTGGSSVTSCLVKGY 169  
 QY 181 FPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSTLGTQTYICNVNHPKSN 240  
 DB 170 FPEPVTVWNSGSLSSVHTLQALQSLGYTMSSVTVPSSTQVTVTCVNHAPASST 229  
 QY 241 KVDKAPKSCDKT-HTCPP-----CPAPELLGQPSVFLPPPKPKDTLMISRTPEVTCV 293  
 DB 230 TVDKLEPSPGPISTINPCPCPECKECHKCAPNLEGGPSVFIPEPNIKDVLMLSTPKVTCV 289  
 QY 294 VVDVSHEDPEVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVHLQDQLNGKEYCKK 353  
 DB 290 VVDVSEDDPDQVLSWFWNNVEVHTAQTQTHREDYNTSTIRVVTLPVQHQQDMSGKEFKCK 349  
 QY 354 VSKALPAPIETKISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWE 413  
 DB 350 VNNKDLSPPIETISKIKGLVRAPQVYILPPAEQLSKQVSLTCLVVGPNPGDISVET 409  
 QY 414 SNGQPNYKTTTPVLDSDGSPFLSKLTVDKSRWQQGNVPSVCSVMHEALHNHYTOKSL 473  
 DB 410 SNGTEENYKDTAPVLDSDGSPFIYKLNMTSKWEKTDSPSCNVRHEGLKNLYLTKTIS 469  
 QY 474 LSPGK 478  
 DB 470 RSPGK 474  
 RESULT 13  
 S01321  
 Ig gamma-2b chain precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
 C:Accession: S01321  
 R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
 Eur. J. Biochem. 176, 287-295, 1988  
 A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed ag  
 A:Reference number: S01320; MUID:88329081; PMID:3138116  
 A:Accession: S01321  
 A:Molecule type: mRNA  
 A:Residues: 1-475 <DE1>  
 A:Cross-references: EMBL:X13188; NID:G51780; PIDN:CAA31580.1; PID:G51781  
 A:Note: this sequence was determined from the differentiated gene  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
 F:159-223/Domain: immunoglobulin homology <IMM>  
 Query Match 52.3%; Score 1338.5; DB 2; Length 475;  
 Best Local Similarity 53.8%; Pred. No. 5.5e-72;  
 Matches 262; Conservative 73; Mismatches 131; Indels 21; Gaps 6;  
 QY 1 MGWSLLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60  
 DB 1 MEWSWIFLLSGTAGVQSQVQLQSGAELARPGASVVKLSCKASGYTLTSYGISWVKQRT 60  
 QY 61 GKGPEWVGFIKPNKGGTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYVCTTS 120  
 DB 61 QGGLWIGYI--YPGSGNSYFNEKFKGKATLTVDKSSSTAYLHLSLTSDESAVYFC--- 115  
 QY 121 YISHCRGGVCYGVY--FEPWGGALVTYSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVK 178  
 DB 116 -----AGPRQVGLLPFGYWGQGLTVTAAAKTTPPSVYPLAPGCGDTTGGSSVTLGCLVK 169  
 QY 179 DYFPEPVTVWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSTLGTQTYICNVNHPKPS 238  
 DB 170 GYPESVTVWNSGSLSSVHTFPAVLQ--SGLYTMSSSVTVPSSTQVTVTCVSAHPAS 228  
 QY 239 NTKVDKKAEPKCDKT-HTCPP-----CPAPELLGQPSVFLPPPKPKDTLMISRTPEVT 291

QY 476 PGK 478  
Db 470 PGK 472

## RESULT 10

S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687; PMID:7744049  
A:Accession: S69339  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:CROSS-references: EMBL:X81695  
R:Khamilichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', 142-374 <KH2>  
A:CROSS-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 55.3%; Score 1415; DB 2; Length 374;  
Best Local Similarity 60.2%; Pred. No. 1.3e-76;  
Matches 286; Conservative 25; Mismatches 52; Indels 112; Gaps 6;  
QY 8 LFLVAVATVQCEVQLVSGGLVQPGSLRVSCAVSGFTFSDH--YMWFRQAPGKGP 65  
Db 8 LLLLTIPSWLVOITLKEGFLVLPKPTQTLTCTFSGFLSKSGVGVGWRQPGQALE 67  
QY 66 WVGFINRKNPGGTTEYAAASVKDRFTISRDSKSIAYLOWSSLIKIEDTAVYCTTSYISHC 125  
Db 68 WLALIFWDDD---KRYSPSLRFLTITKTSKNQVLTWNVDPADTATYICGVISVEG-- 122  
QY 126 RGVCVYG-GY-REFWQAGALVTVSSASTKGPVFLPAPSSKTSKGGTAALGLCKVNDYPP 183  
Db 123 -----YGCQYRFHSGQGLTVTVSS----- 142  
QY 184 PVTVSNWNSGALTSVGHVTFPAVLQSSGLYLSLVSVTVVPSSSLGTQTYICNVNHKPSNTKVD 243  
Db 143 ----- 142  
QY 244 KKAEPKCDKTHTCPPCAPPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPE 303  
Db 143 ---EPKSCDKTHTCPPCAPPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPE 199  
QY 304 VKFNWTVGVGVHNAKTPREQYNSTYRVWSVLTVLHODWLNKEYKCKVSNKALPAPI 363  
Db 200 VKFNWTVGVGVHNAKTPREQYNSTYRVWSVLTVLHODWLNKEYKCKVSNKALPAPI 259  
QY 364 EKTISKAKGQPREPQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYK 423  
Db 260 EKTISKAKGQPREPQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYK 319  
QY 424 TTPPVLDSDGSGFLYSKLTVDKSRWQQGNVFCSVWHEALHNHYTQKSLSLSPGK 478  
Db 320 TTPPVLDSDGSGFLYSKLTVDKSRWQQGNVFCSVWHEALHNHYTQKSLSLSPGK 374

## RESULT 11

S40295  
Ig gamma-2a chain (mAb735) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 16-Jul-1999  
C:Accession: S40295

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Froesch, M.; Weisgerber, C.; Bit  
submitted to the EMBL Data Library, January 1993  
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against  
A:Reference number: S40295  
A:Accession: S40295  
A:Molecule type: protein  
A:Residues: 1-446 <KLE>  
C:Genetics:  
A:Map position: 12  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglyutamic acid  
F;1-446/Product: Ig gamma-2a chain #status experimental <MA>  
F;1-117/Domain: V-D-J region <VDU>  
F;118-446/Domain: C region <CHR>  
F;118-214/Domain: C1 region <CH1>  
F;215-230/Region: hinge  
F;231-340/Domain: C2 region <CH2>  
F;341-446/Domain: C3 region <CH3>  
F;360-427/Domain: immunoglobulin homology <IMW>  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted  
F;132/Disulfide bonds: interchain (to light chain) #status predicted  
F;224,227,229/Disulfide bonds: interchain #status predicted  
F;297/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 55.3%; Score 1415; DB 2; Length 446;  
Best Local Similarity 58.0%; Pred. No. 1.6e-76;  
Matches 268; Conservative 69; Mismatches 105; Indels 20; Gaps 6;

QY 20 EVQLVESGGGLVQPGSLRVSCAVSGFTFSDHYWFRQAPGKGPWVGFINRKNPGGTT 79  
Db 1 QIQLOQSGPGLVRFPGASVKISKASGYTFTDYIHWVKQRPGELEWIGWI--YPGSGNT 58  
QY 80 EYAAASVKDRFTISRDSKSIAYLOWSSLIKIEDTAVYCTTSYISHCRGGVCVGGYF--EF 137  
Db 59 KYNEKFKGKATLTVDTSSSTAYNQLSLSLTSSEDSAVYFCAR-----GGKFAMDY 106  
QY 138 WGQGALVTVSSASTKGPVFLPAPSSKTSKGGTAALGLCKVDFPPEPVTVMNSGALTSG 197  
Db 107 WGQGTSVTSSAKTTPAPVYPLAPVCGDITGSSVTLGCLVKGYFPEPVTLTWNSGSLSSG 166  
QY 198 VHTFPAVLQSSGLYLSLVSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC 257  
Db 167 VHTFPAVLQSD-LYTLSSSVTVTSTWPSQSIITCNVAHPASSTKVDKKTIEPRG-PTIKPC 224  
QY 258 PP--CPAPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 315  
Db 225 PPCKCAPNLLGGPSVFIFFPKIKDVLMSLSLSPWVTCVVVDVSEDDPDVQISWFWNVVEV 284  
QY 316 HNAKTPREEQYNSTYRVWSVLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQPR 375  
Db 285 LTAQTQTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVR 344  
QY 376 EPQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPTPVLDSDGSGF 435  
Db 345 APQVYVTLPPPEEEMTKQVTLTCWVDFMPEDIYVEWTNNGKTELNYKNTPEVLDSDGSY 404  
QY 436 FLYSKLTVDKSRWQQGNVFCSVWHEALHNHYTQKSLSLSPG 477  
Db 405 FMYSKURVEKKNWERNVNSCSVWHEGLHNHHTTKFSRTPG 446

## RESULT 12

G2WS11  
Ig gamma-2b chain - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
C:Accession: S25057; A26235; A26232; A26233; A53598  
R:Fischer, R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific mc  
A:Reference number: S25057  
A:Accession: S25057

Query Match 57.7%; Score 1478; DB 2; Length 470;  
Best Local Similarity 60.9%; Pred. No. 3.1e-80;  
Matches 291; Conservative 58; Mismatches 115; Indels 14; Gaps 7;

QY 3 WSLILLFLAVATRVQCEVOLVESGGGLVOPGSLRVSCAVSGFTFSDHYMYWFRQAPGK 62  
DB 5 WT--LLFVLSPAGVLSQVQLRESGSLVPSQTLSTCTVSGFSLSYALTWRQAPGK 62  
QY 63 GPEWVGFIKPNKNGGTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYCTT 122  
DB 63 ALEWVGGI---TSGGTYYNPALKKRLSITKENSQSQVLSVSSVTPEDTATYYCARS-- 117  
QY 123 SHCRGGVCYGGYFEPWGGQALVTVSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFP 182  
DB 118 --TYEVDGGAIDAWGQGLLTVVSASTAPKVPYLSGCCDKSSSTVTLGCLVSSYMP 175  
QY 183 EPTVSWNSGALTSVGHVTPPAVLQSSGLSYLSVTVTPSSSLGTQYICNVNHPKSNTKV 242  
DB 176 EPTVWNSGALKSGVHTFPAVLQSSGLSYLSVTVTPGSTG--QFTCNVAHPASSTKV 234  
QY 243 DKKAPKSCDKTHTCPPCPAPELLGPGSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDP 302  
DB 235 DKAVDP-TC-KPSPDCDCCPPPELPGSPSVFIPPKPKDTLISGTPVTCVVVDVGHDDP 292  
QY 303 EVKFNWYDGVVEVHNAKTPREEQNSTYRVVSVTLVHODWLNKGEYKCKVSNKALPAP 362  
DB 293 EVKFNWYDGVVEVHNAKTPREEQNSTYRVVSVTLVHODWLNKGEYKCKVSNKALPAP 352  
QY 363 IEKTSKAGQPREPOVNTLPSPRDELTKNOVSLCLVKGFYFSPSDIAVWESNGOP--EN 420  
DB 353 IVRTISRTKGPAREQVYVLPAPQBELSKSTVSLTCMTWTSFYPDYIAVWQNGQPESED 412  
QY 421 NYKTTPPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 478  
DB 413 KYGTTPPQLDASSYFLYSLKLVDRNSQEGDTYTCVWHEALHNHYTKQSLSPGK 470

RESULT 8  
S37483  
IG Gamma-2a chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
R:Ducancel, F.F.D.  
A:Accession: S37483  
A:Reference number: S37483  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-469 <DUC>  
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 57.3%; Score 1467.5; DB 2; Length 469;  
Best Local Similarity 57.7%; Pred. No. 1.3e-79;  
Matches 277; Conservative 72; Mismatches 118; Indels 13; Gaps 5;

QY 1 MGWSLILLFLAVATRVQCEVOLVESGGGLVOPGSLRVSCAVSGFTFSDHYMYWFRQAP 60  
DB 1 MGWSLIFLLSGTAGVHCQIQLOQSGPELVKPGASVKISCKASGTYTDTYYINWVKQP 60  
QY 61 GKEPVGFIKPNKNGGTTEYAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYCTTS 120  
DB 61 GGLKWIWI--YPASGNTKYNENFKGATLTVDTSSATMQLSSLTSEDATVYFC--- 115  
QY 121 YISHCRGGVCYGGYFEPWGGQALVTVSASTKGPSVPLAPSSKSTSGGTAALGCLVKDY 180  
DB 116 ----ARAMGATATLLDYGQGTTLTVSSAKTTPASVYPLAPVCGDTGSSVTLGCLVKGY 171  
QY 181 FPEPTVWNSGALTSVGHVTPPAVLQSSGLSYLSVTVTPSSSLGTQYICNVNHPKSN 240

Db 172 FPEPTVTLWNSSGLSGVHTFPAVLQSD-LYTLSSSVTVTSSWPSQSLTCNVHPASST 230  
QY 241 KVDKAPKSCDKTHTCPP--CPAPELLGPGSVFLPPPKPDKTLMISRTPEVTCVVVDVS 298  
DB 231 KVDKIEPRG-PTIKPCPPCCPAPNLGPGSVFIPPKIKDVLMLSLSPITVTCVVVDVS 289  
QY 299 HEDPEVKFNWYDGVVEVHNAKTPREEQNSTYRVVSVTLVHODWLNKGEYKCKVSNKA 358  
DB 290 EDDPDVQISWFNWVNNVEHTAQQTQTHREDYNSTLRVVSALPIQHODWMSGKFKCKVNNKD 349  
QY 359 LPAPIEKTSKAGQPREPOVNTLPSPRDELTKNOVSLCLVKGFYFSPSDIAVWESNGOP 418  
DB 350 LPAPIERTISKGPSVRAPQVYVLPPEBEWTKQVTLTCMTWDFPEDIYVWNTWNGKT 409  
QY 419 ENNYKTTTPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 478  
DB 410 ELNFKNTEPVLDSGSPFMYKSLRVEKONWVERNSYSCSVWHEGLNHHHTTKFSFRTPGK 469

RESULT 9  
S31459  
IG gamma-1 chain - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S31459  
R:Patric, S.; Nau, F.  
A:Reference number: S31459  
A:Accession: S31459  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-472 <PAT>  
A:Cross-references: EMBL:X69797  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 55.8%; Score 1429; DB 2; Length 472;  
Best Local Similarity 58.4%; Pred. No. 2.5e-77;  
Matches 282; Conservative 63; Mismatches 118; Indels 20; Gaps 9;

QY 3 WSLILLFLAVATRVQCEVOLVESGGGLVOPGSLRVSCAVSGFTFSDHYMYWFRQAPGK 62  
DB 3 WT--LLFVLSPAGVLSQVQLRESGSLATLQTLSTVCTISGFLSNLYGVDVWVQAPGK 60  
QY 63 GPEWVGFIKPNKNGGTTE--YAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYCT- 118  
DB 61 ALEWLG-----CSGDEDEDYNPVLKSLSLITKDTSKQVSLTSLVTTEDTAVYICAR 114  
QY 119 TSY-ISHCRGGVCYGGYFEPWGGQALVTVSASTKGPSVPLAPSSKSTSGGTAALGCLV 177  
DB 115 VDYDSSH--APAYASY-DFWGPGLLSVLSASTTPKVPVPLTSCCGDTSSSIVTLGCLV 170  
QY 178 KDYPPEPTVWNSGALTSVGHVTPPAVLQSSGLSYLSVTVTPSSSLGTQYICNVNHP 237  
DB 171 SSTMPEPTVTVWNSGALTSVGHVTPPAILOSSGLSYLSVTVTPASTSGAQTFCNVAHPA 230  
QY 238 SNTKVKKAPKSCDKTHTCPPCPAPELLGPGSVFLPPPKPDKTLMISRTPEVTCVVVDV 297  
DB 231 SSTKVKDRVEPCDPCKKC-RCPPPELPGSPSVFIPPKPKDTLISGTPVTCVVVDV 289  
QY 298 SHEDPEVKFNWYDGVVEVHNAKTPREEQNSTYRVVSVTLVHODWLNKGEYKCKVSNK 357  
DB 290 QODDPEVQFSWFVDNVEVHTARTKPREEQFNSTFRVVSALPIQHODWTKGKFKCKVHNE 349  
QY 358 ALPAPIEKTSKAGQPREPOVNTLPSPRDELTKNOVSLCLVKGFYFSPSDIAVWESNGQ 417  
DB 350 ALPAPIVRTISRTKGPAREQVYVLPAPQBELSKSTVSLTCLVTFYGYPIYIAVWQNGQ 409  
QY 418 P--BNVKTTPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSL 475  
DB 410 PESEDKYGTTSQLDADGSYFLYSLRVRVDRNSWQEGDTYACVWHEALHNHYTKQSL 469

A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A:Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant  
A:Reference number: A90249; MUID:70207560; PMID:4192699  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30;81-326 <FIN>  
C:Genetics:  
A:Gene: GDB:IGHG4  
A:Cross-references: GDB:1119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-303/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:117/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.9%; Score 1586.5; DB 1; Length 327;  
Best Local Similarity 90.6%; Pred No. 8.1e-87;  
Matches 299; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

Qy 149 ASTKGPVFLPLAPSSKSTGGTAALGCLVKDYFPEPTVTVSNWNSGALTSQVHTTPAVLQSS 208  
Db 1 ASTKGPVFLPLAPSSKSTGGTAALGCLVKDYFPEPTVTVSNWNSGALTSQVHTTPAVLQSS 60  
Qy 209 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCCPPAPELGG 268  
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCCPPAPELGG 117  
Qy 269 PSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVVHNAKTKPREQYN 328  
Db 118 PSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVVHNAKTKPREQYN 177  
Qy 329 STYRVSVLVTLHODWLNKGEYKCKVSNKALPAPIETKSIAKQPREPQVYTLPPSRDE 388  
Db 178 STYRVSVLVTLHODWLNKGEYKCKVSNKALPAPIETKSIAKQPREPQVYTLPPSQEE 237  
Qy 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 448  
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 297  
Qy 449 QOQNVFSCVWVHNAHNYTKQSLSPGK 478  
Db 298 QOQNVFSCVWVHNAHNYTKQSLSPGK 327

RESULT 6  
FC4436  
monoclonal antibody 13-1 heavy chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
C:Accession: PC4436  
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr  
A:Reference number: JCS810; MUID:98063277; PMID:9398605  
A:Accession: PC4436  
A:Molecule type: protein  
A:Residues: 1-444 <AKA>  
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:251-320/Domain: immunoglobulin homology <IMM>  
F:22/Disulfide bonds: interchain (to 98) #status predicted  
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 58.4%; Score 1494.5; DB 2; Length 444;  
Best Local Similarity 60.5%; Pred No. 3.1e-81;  
Matches 279; Conservative 68; Mismatches 95; Indels 19; Gaps 6;

Qy 20 EVOLVESGGLVQPGSLAVSCVSGGTFSDHYMYWFRQAPGKGPWGFIRKPNKGGTT 79  
Db 1 EVQXVETGGGLVRPGNSLKLSTSGFTFSYRHMHLRQPPGKRLEWIAVITVKSDNYGA 60  
Qy 80 EYAAASKDRFTTISRDDSKSIAYLQMSLSKIEDTAVYCTTTSYSHCRGGVCYGYFEFG 139  
Db 61 KYAESVGRFTTISRDDSKSVLYQMLRLREEDTATYTC-----CRTPWVYA--MDCWG 111  
Qy 140 QGALVTVSSASTKGSVPLAPSSKSTGGTAALGCLVKDYFPEPTVTVSNWNSGALTSQVH 199  
Db 112 QGTSVIVSSAKTTPSVVPLAPGSAQAQNSMTVGLCLVKGYFPEPTVTVSNWNSGALTSQVH 171  
Qy 200 TPAVLOSSLGLVLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCCPP 259  
Db 172 TPAVLOSSLGLVLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCCPP 226  
Qy 260 --CPAPELGGSPSVFLPPPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVVH 317  
Db 227 CICTVPEV---SSVFIFFPKPKDVLITLTTPKVTGVVDISKDDPEVQFSWFVDDVEVHT 283  
Qy 318 AKTKPREEOYNTYRVSVLVTLHODWLNKGEYKCKVSNKALPAPIETKSIAKQPREP 377  
Db 284 AQTPREEOYNTYRVSVLVTLHODWLNKGEYKCKVSNKALPAPIETKSIAKQPREP 343  
Qy 378 QVTLPPSRDELTQKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFL 437  
Db 344 QVTLPPSRDELTQKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFL 403  
Qy 438 YSKLTVDKSRWQOQNVFSCVWVHNAHNYTKQSLSPGK 478  
Db 404 YSKLTVDKSRWQOQNVFSCVWVHNAHNYTKQSLSPGK 444

RESULT 7  
S22080  
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine  
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S22080; S06610; A31303  
R:Sanders, P.G.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S22080  
A:Accession: S22080  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-470 <SAN>  
A:Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440  
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
Mol. Immunol. 26, 841-850, 1989  
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma  
A:Reference number: S06610; MUID:90097956; PMID:2513487  
A:Accession: S06610  
A:Molecule type: DNA  
A:Residues: 142-470 <SYM>  
A:Cross-references: EMBL:X16701  
A:Note: the sequence was determined from the germline gene  
C:Genetics:  
A:Gene: Ig CH gamma-1  
A:Introns: 98/1; 111/1; 221/1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
F:161-225/Domain: immunoglobulin homology <IMM>  
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

A.Molecule type: protein  
A.Residues: 239-275 <HOF>  
R.Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A.Reference number: A94591  
A.Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A.Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
end

R.Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A.Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A.Reference number: A90253; MUID:72033500; PMID:4940472  
A.Contents: annotation; myeloma protein Sa, disulfide bonds  
R.Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A.Title: Structural studies of immunoglobulin G.  
A.Reference number: A93157; MUID:59064124; PMID:5782707  
A.Contents: annotation; Sa, disulfide bonds  
C.Genetics:  
A.Gene: GDB:IGHG2  
A.Cross-references: GDB:119338; OMIM:147110  
A.Map position: 14q32.33-14q32.33  
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into kap  
C.Superfamily: immunoglobulin C region; immunoglobulin homology  
C.Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.5%; Score 1600; DB 1; Length 326;  
Best Local Similarity 90.9%; Pred. No. 1.3e-87;  
Matches 300; Conservative 12; Mismatches 14; Indels 4; Gaps 2;

QY 149 ASTKGPSVFPLAPSSKSTSGGTALGLVKDYFPEPTVSNWGALTSGVHTFPAVLQSS 208  
DB 1 ASTKGPSVFPLAPCSRSTSESTAALGLVKDYFPEPTVSNWGALTSGVHTFPAVLQSS 60  
QY 209 GLYSLSVVTVSSSLGQTQYICNVNHPKSTKVDKKAEPKSCDKTHTCPCPAPELLGG 268  
DB 61 GLYSLSVVTVSSNFGQTQYTCNVDPKPSNTKVDKTKVERKCCVE---CPCPAPP-VAG 116  
QY 269 PSVFLPPPKDQTLIMISPTPTCTCVVDVSHEDPEVKFNWYVDGVVHNATKTPRESQYN 328  
DB 117 PSVFLPPPKDQTLIMISRPEVTCVVDVSHEDPEVGNWYVDGVVHNATKTPRESQFN 176  
QY 329 STYRVVSVLTVLHDLNMGKEYCKVSNKALPAPIETISKAKQPREPQVYTLPPSRDE 388  
DB 177 STYRVVSVLTVLHDLNMGKEYCKVSNKGLPAPIETISKTKQPREPQVYTLPPSRDE 236  
QY 389 LTKNVSVLTCLVKGPYPSPDIAVEVESNGQPNNTKTPPPVLDSDGSPFLYSKLTVDKSRW 448  
DB 237 MTKNVSVLTCLVKGPYPSPDIAVEVESNGQPNNTKTPPPVLDSDGSPFLYSKLTVDKSRW 296  
QY 449 QQGNVFSCSVHAEALHNHYTQKSLSLSPGK 478  
DB 297 QQGNVFSCSVHAEALHNHYTQKSLSLSPGK 326

RESULT 5  
G4HU  
Ig Gamma-4 chain C region - human  
C.Species: Homo sapiens (man)  
C.Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 16-Jul-1999  
C.Accession: A90933; A90249; A02150  
R.Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A.Title: Nucleotide sequence of a human immunoglobulin C-gamma 4 gene.  
A.Reference number: A90933; MUID:83157104; PMID:6299662

igen Primerstruktur.  
A;Reference number: A91668; MUID:77070269; PMID:826475  
A;Contents: myeloma protein Nie  
A;Accession: B91668  
A;Molecule type: protein  
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A;Note: this sequence has the G1m(17) and G1m(1) markers  
R;Schmidt, W.E.; Jung, H.D.; Falm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A;Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI  
A;Reference number: A91723; MUID:83289131; PMID:6884994  
A;Contents: myeloma protein KOI; disulfide bonds  
A;Accession: A91723  
A;Molecule type: protein  
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A;Note: this sequence has the G1m(3) and G1m(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A;Reference number: A90565; MUID:71064027; PMID:4923144  
A;Contents: annotation; disulfide bonds  
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A;Reference number: A91667; MUID:77070267; PMID:1002129  
A;Contents: annotation; disulfide bonds  
C;Genetics:  
A;Gene: GDB:IGHG1  
A;Cross-references: GDB:120085; OMIM:147100  
A;Map position: 14q32.33-14q32.33  
A;Introns: 99/1; 114/1; 224/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;137-206/Domain: immunoglobulin homology <IM2>  
F;243-310/Domain: immunoglobulin homology <IM3>  
F;27-83,144-204,250-308/Disulfide bonds: #status experimental  
F;103/Disulfide bonds: interchain (to light chain) #status experimental  
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 68.8%; Score 1763; DB 1; Length 330;  
Best Local Similarity 99.7%; Pred. No. 3e-97; Mismatches 1; Indels 0; Gaps 0;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 149 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 208  
Db 1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60

Qy 209 GLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPPKVTPPPVSLTCLVK 268  
Db 61 GLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKKAEPPKVTPPPVSLTCLVK 120

Qy 269 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYN 328  
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYN 180

Qy 329 STYRVSVSLTVLHQDLWGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTPPSSRDE 388  
Db 181 STYRVSVSLTVLHQDLWGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTPPSSRDE 240

Qy 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 448  
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy 449 QGQNVFSCSVMEALHNHYTQKSLSLSPCK 478  
Db 301 QGQNVFSCSVMEALHNHYTQKSLSLSPCK 330

RESULT 2  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C;Accession: A23511  
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con  
A;Reference number: A23511; MUID:86148507; PMID:3081877  
A;Accession: A23511  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
A;Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056  
C;Genetics: GDB:IGHG3  
A;Cross-references: GDB:119339; OMIM:147120  
A;Map position: 14q32.33-14q32.33  
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 1626.5; DB 2; Length 377;  
Best Local Similarity 81.7%; Pred. No. 4.1e-89;  
Matches 308; Conservative 10; Mismatches 12; Indels 47; Gaps 1;

Qy 149 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 208  
Db 1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60

Qy 209 GLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKKA----- 246  
Db 61 GLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKRELKTPGLDTHTCRCPEPKSC 120

Qy 247 -----EPKSCDKTHCTCPCPAPELGGPSVFLPPPKPKDT 281  
Db 121 DTPPPCPCRCPEPKSCDTPPPCPCRCPEPKSCDTPPPCPCRCPELGGPSVFLPPPKPKDT 180

Qy 282 LMTSRPTVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYNSTYRVSVSLTVLH 341  
Db 181 LMTSRPTVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEOYNSTYRVSVSLTVLH 240

Qy 342 QDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTPPSSRDELTKNQVSLTCLVK 401  
Db 241 QDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYVTPPSSRDELTKNQVSLTCLVK 300

Qy 402 GFYPDSIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNFSCSVMEH 461  
Db 301 GFYPDSIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNFSCSVMEH 360

Qy 462 ALHNHYTQKSLSLSPCK 478  
Db 361 ALHNHYTQKSLSLSPCK 377

RESULT 3  
A60764  
Ig gamma-3 chain C region, form LAT - human  
C;Species: Homo sapiens (man)  
C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999  
C;Accession: A60764  
R;Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A;Title: A human immunoglobulin IGHG3 allele (Gmb0. b1, c3, c5, u) with an IGHG4 convert  
A;Reference number: A60764; MUID:90007613; PMID:2571587  
A;Accession: A60764  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

GenCore version 5.1.4 p5 4578  
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OM protein - protein search, using sw model

Run on: March 29, 2003, 09:06:24 ; Search time 21.453 Seconds  
(without alignments)  
2141.995 Million cell updates/sec

Title: US-09-758-173-8

Perfect score: 2561

Sequence: 1 MGWSLLFLFVAVTRVQCE.....MHEALHNYTKSLSLSPCK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1763	68.8	330	1 GHU	Ig gamma-1 chain C
2	1626.5	63.5	377	2 A23511	Ig gamma-3 chain C
3	1624.5	63.4	377	2 A60764	Ig gamma-3 chain C
4	1600	62.5	326	1 G2HU	Ig gamma-2 chain C
5	1586.5	61.9	327	1 G4HU	Ig gamma-4 chain C
6	1494.5	58.4	444	2 PC4436	monoclonal antibody
7	1478	57.7	470	2 S22080	Ig heavy chain pre
8	1467.5	57.3	469	2 S37483	Ig gamma-2a chain
9	1429	55.8	472	2 S31459	Ig gamma-1 chain -
10	1415	55.3	374	2 S69339	Ig heavy chain v r
11	1415	55.3	446	2 S40295	Ig gamma-2a chain
12	1392	54.4	474	1 G2MS11	Ig gamma-2b chain
13	1338.5	52.3	475	2 S01321	Ig gamma-2a chain
14	1259	49.2	328	2 I47159	Ig gamma-2a chain
15	1256	49.0	255	4 S31866	Ig gamma-1 chain C
16	1253	48.9	328	2 I47160	Ig gamma-2b chain
17	1250	48.8	234	2 PT0207	Ig gamma chain C r
18	1227	47.9	328	2 I47158	Ig gamma-1 chain C
19	1226.5	47.9	323	1 GHRB	Ig gamma chain C r
20	1223	47.8	328	2 I47161	Ig gamma-3 chain C
21	1212.5	47.3	329	1 G2GP	Ig gamma-2 chain C
22	1157.5	45.2	308	2 C30554	Ig heavy chain C r
23	1152	45.0	289	1 G3HUM1	Ig gamma-3 heavy c
24	1148	44.8	326	2 PS0017	Ig gamma-1 chain C
25	1142.5	44.6	334	2 PS0018	Ig gamma-2b chain
26	1138	44.4	323	1 GMS	Ig gamma-1 chain C
27	1137	44.4	329	1 G3MSC	Ig gamma-3 chain C
28	1133	44.2	393	1 G1MSC	Ig gamma-1 chain C
29	1126	44.0	398	1 G3MSM	Ig gamma-3 chain C

## ALIGNMENTS

### RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999

C:Accession: A93433; S3887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, 2

A:Note: Lys-330 is removed after translation

R:Harrie, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a c

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Note: This sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'O',156-165,'O',178-194,'N',196-197,'D',199-238,'E',240,'

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),









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; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343,485A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 18986
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: referred to as "Molly"
US-09-343-485A-2

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Query Match 78.5%; Score 1127.4; DB 4; Length 18986;  
Best Local Similarity 87.8%; Pred. NO. 5e-260;  
Matches 1262; Conservative 0; Mismatches 151; Indels 24; Gaps 2;

Qy	1	ATGGGTTGAGGCTCATCTTGTCTCTCTTGTTCGCTGTGTGCTACGCGTGTCCAGTGTGAG	60
Db	9433	ATGGGTTGAGGCTCATCTTGTCTCTCTTGTTCGCTGTGTGCTACGCGTGTCTGTCTCCGAC	9492
Qy	61	GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTTCAGCGCTGGCGGTCCTCTGAGAGTCTCC	120
Db	9493	GTAACAATTCGAGGCTGGGCTGAGCTGTGTGAAGCCTCGGGGCTCAGTGAAGATGTCC	9552
Qy	121	TGTGCAAGTCTCTGGATTCACTTTCAGTGACCACTACATGTAATTGGTTCCGCGCAGGCTCCA	180
Db	9553	TGCAAGGCTTCTGGCTACACATTTACCAAGTTTACAATATGCACATGGGTAAACAGACACCT	9612
Qy	181	GGGAAGGGCGGGAATGGGTAGGTTTCATTAGAAACAAACCGAACGGTGGGGAACAACAGAA	240
Db	9613	GGTGGGGGCTGGAATGGAATTGGAGCTATT-----TATCCCGGAAATGGTGATCTTCC	9666
Qy	241	TACGCCGCTCTGTGAAGACAGATTCACCATCTCCAGAGATGATTCCAAAGCAGCTGCC	300
Db	9667	TACAATCAAGAATTCAAGGCAAGGCCACATTTGACTGCAGACAAATCCTCCAGCACAGCC	9726
Qy	301	TATCTCAAAATGAGACAGCCTGAAAAATCGAGGACACGGCGGCTATTACTGTACTACATCC	360
Db	9727	TACATGCACTCAGCAGCCTGCATCTGAGGACTCTGGGCTATTACTGTGCAAGATC-	9785
Qy	361	TACATTTCAATTGTGGGGTGGTGTCTGCTATGAGAGTTACTTCGAATCTTGGGGCCAG	420
Db	9786	-----GACTTACTACGGCGTGACTGTGTTCAATGTCTGGGGCGCA	9828
Qy	421	GGGGCCCTGGTCACGGTCTCTCAGCTAGCAACAAAGGGCCCATCGGTCTTCCCGCTGGCA	480
Db	9829	GGGACCACGGTCACCGTCTCTGCAGCTAGCAACAAAGGGCCCATCGGTCTTCCCGCTGGCA	9888
Qy	481	CCCTCTCTCAAGACACCTCTGGGGGCAACGGCCCTGGGCTGCCCTGGTCAAGGACTAC	540
Db	9889	CCCTCTCTCAAGACACCTCTGGGGGCAACGGCCCTGGGCTGCCCTGGTCAAGGACTAC	9948
Qy	541	TTCCCGGAACCGGTGACGGTGTCTGTGGAACCTCAGCGCCCTGACCGAGCGGCTGCACACC	600
Db	9949	TTCCCGGAACCGGTGACGGTGTCTGTGGAACCTCAGCGCCCTGACCGAGCGGCTGCACACC	10008
Qy	601	TTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCTCTCAGCAGCGTGGTGAACGTGCC	660
Db	10009	TTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCTCTCAGCAGCGTGGTGAACGTGCC	10068
Qy	661	TCCAGCAGCTTGGGCAACCAACCTTACATCTGCAACGTGTAATCACAGGCCCAACACACC	720
Db	10069	TCAGCAGCTTGGGCAACCAACCTTACATCTGCAACGTGTAATCACAGGCCCAACACACC	10128
Qy	721	AAGGTGGAACAAGAAAGCAGAGCCCAATCTTTGTGACAAAATCTCACATATGCCACCGTGC	780

Db	10129	AGGTGGACAGAAAGACAGACCCAAATCTTTGACAAAACTCACATGCCACCGTC	10188
Qy	781	CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAGGAC	840
Db	10189	CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAGGAC	10248
Qy	841	ACCTCATGATCTCCGGACCCCTGAGGTCAATGCGTGGTGGTGTGACGTGAGCCAGAA	900
Db	10249	ACCTCATGATCTCCGGACCCCTGAGGTCAATGCGTGGTGGTGTGACGTGAGCCAGAA	10308
Qy	901	GACCTGAGGTCAAGTTCAA CTGGTACGTGGACGGCGTGGAGTGCATAATGCCAAGACA	960
Db	10309	GACCTGAGGTCAAGTTCAA CTGGTACGTGGACGGCGTGGAGTGCATAATGCCAAGACA	10368
Qy	961	AAGCCGCGGGAGGACGAGTCAACAGCACGTAACCGTGTGGTCAGCGTCTCTCACCGTCTGT	1020
Db	10369	AAGCCGCGGGAGGACGAGTCAACAGCACGTAACCGTGTGGTCAGCGTCTCTCACCGTCTGT	10428
Qy	1021	CACAGGACTGCTGAATGGCAAGGATGACAAAGTGCAGGTCTTCCAAACAAAGCCCTCCCA	1080
Db	10429	CACAGGACTGCTGAATGGCAAGGATGACAAAGTGCAGGTCTTCCAAACAAAGCCCTCCCA	10488
Qy	1081	GCCCCATCGAGAAAACCATCTTCCAAAGCCAAAGGCGAGCCCGAGAACCAAGCTGTAC	1140
Db	10489	GCCCCATCGAGAAAACCATCTTCCAAAGCCAAAGGCGAGCCCGAGAACCAAGCTGTAC	10548
Qy	1141	ACCTGCCCCCATCCCGGATGAGTGCACAAAGAACAGGTTCAGCCTGACCTGCCTGGTCT	1200
Db	10549	ACCTGCCCCCATCCCGGATGAGTGCACAAAGAACAGGTTCAGCCTGACCTGCCTGGTCT	10608
Qy	1201	AAAGGTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGCAATGGGAGCCGAGAAC	1260
Db	10609	AAAGGTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGCAATGGGAGCCGAGAAC	10668
Qy	1261	AACTACAGACACACGCTCCCGTCTGGACTCCGACGGTCTCTTCTCTCTACAGCAAG	1320
Db	10669	AACTACAGACACACGCTCCCGTCTGGACTCCGACGGTCTCTTCTCTCTACAGCAAG	10728
Qy	1321	CTCACCGTGGACAAAGACAGGTGGCAGCGGGGAAAGTCTTCTCATGCTCCCGTGATGCAT	1380
Db	10729	CTCACCGTGGACAAAGACAGGTGGCAGCGGGGAAAGTCTTCTCATGCTCCCGTGATGCAT	10788
Qy	1381	GAGGCTCTGCACAAACCACTACACGAGAGAGGCTCTCTCTGTCTCCGGGTAATGA	1437
Db	10789	GAGGCTCTGCACAAACCACTACACGAGAGAGGCTCTCTCTGTCTCCGGGTAATGA	10845

RESULT 13

US-09-027-449-68

; Sequence 68, Appli

Sequence 00, Application 00/0002, Patent No. 6025158

; GENERAL INFORMATION:

APPLICANT: Gonzalez, Tania R.

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

**TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and**

**TITLE OF INVENTION:** Humanized Anti-IL-8 Monoclonal Antibodies

; NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA way

CITY: South San Francisco  
STATE: CaliforniaSTATE: Calif  
COUNTRY: USA

COUNTRY: USA  
ZTD: 94080

; ZIP: 94080  
; COMPUTER READABLE FORM.

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 5 inch, 1 44 Mb floppy disk

MEDIUM TYPE: 3.5 INCH, 1.44 MB  
COMPUTER: IBM PC compatible

COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS/MS-DOS

! OPERATING SYSTEM: PC-DOS/MS-DOS  
! SOFTWARE: WinPatIn (Genentech)

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; SOFTWARE.  WINFACTS (SEMENTECH)
;
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/027,449

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: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/023,715
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/819,866
: FILING DATE: 14-MAR-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Teskin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-352
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18986 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-09-023-715-2

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Query Match	78.5%;	Score 1127.4;	DB 2;	Length 18986;
Best Local Similarity	87.8%;	Pred. No. 5e-260;		
Matches 1262;	Conservative 0;	Mismatches 151;	Indels 24;	Gaps
QY	1	ATGGTTGGAGCCTCATCTGCTCTCTCCCTGCTGCGCTGTGCTACCGCTGTCAGTGTGAG	60	
Db	9433	ATGGTTGGAGCCTCATCTGCTCTCTCCCTGCTGCGCTGTGCTACCGCTGTCAGTGTGAG	60	
QY	61	GTCCAACTCGTGTGGAGTCTGGGGGAGGCTTGGTCCAGCCCTGGCGGTCCCTCGAGAGTCTCC	120	
Db	9493	GTAACTCGCAGCAGCTGGGGCTGAGCTGTGTGAGCCTGGGGCTCAGTGAAGATGTC	9552	
QY	121	TGTGCAGTCTCTGGATTCACTTCAGTGACCTACATGTATTTGGTTCCGGCAGGCTCCA	180	
Db	9553	TGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCAATGCACTGGGTAAACACAGACCT	9612	
QY	181	GGGAAGGGCGCGAATGGGTAGTTTCATTAGAAACAACCGACGGTGGGACACAGAA	240	
Db	9613	GGTCGGGGCTGGAATGGATGGAGCTATT-----TATCCGGAAATGGTGATCTTC	9666	
QY	241	TACGCCCGCTCTGTGAAGACACAGATTCACCATCTCCAGAGATGATTCCAAAGCATCGCC	300	
Db	9667	TACAATCAGAAGTTCAAAGCAGGCCACATTTGACTGCAGACAAATCTCCAGCAGACCC	9726	
QY	301	TATCTGCAATGAGCAGCCTGAAATCGAGGACACGGCGGCTATTACTGTACTACATCC	360	
Db	9727	TACATCGAGCTCAGCAGCCTGCATCTGAGGACTCTGGGCTATTACTGTGCAAGATC-	9785	
QY	361	TACATTTCAATTGTCGGGTGGTGTCTGCTATGAGGTACTTCGAATTCCTGGGGCCAG	420	
Db	9786	-----GACTTACTACGGCGGTGACTGGTACTTTCAATGCTGGGGCGCA	9828	
QY	421	GGCGCCCTGGTCAACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTCCCGCTGGCA	480	
Db	9829	GGGACCACGGTCACCGTCTCTCGAGTAGCACCAAGGGCCCATCGGTCTTCCCTCGGCA	9888	
QY	481	CCCTCTCCAGAGCACCTCTGGGGGCAACGGCGCCCTGGGCTGCTGGTCAAGGACTAC	540	

Db	9889	CCCTCCTCCAAGAGACACCTCTGGGGGCACAGCGGCCCTGGCTGGTCAAGAGACTAC	9948
Qy	541	TTCCCCGAAACCGGTGACGGTGTGTGGAACTCAGCGGCCCTTGACAGCGGGGTGCACACC	600
Db	9949	TTCCCCGAAACCGGTGACGGTGTGTGGAACTCAGCGGCCCTTGACAGCGGGGTGCACACC	10008
Qy	601	TTCCCGGGTGTCTCTACGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCCGTGCC	660
Db	10009	TTCCCGGGTGTCTCTACGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCCGTGCC	10068
Qy	661	TTCCAGAGTTGGGCACCCAGACCTTACATCTGCAACGTGAATCACAAGCCCAAGCAACACC	720
Db	10069	TTCCAGAGTTGGGCACCCAGACCTTACATCTGCAACGTGAATCACAAGCCCAAGCAACACC	10128
Qy	721	AAGGTGGACAGAAAGACAGACCCAAATCTTTGTGCAAAATCTCACATGCCACCGTGC	780
Db	10129	AAGGTGGACAGAAAGACAGACCCAAATCTTTGTGCAAAATCTCACATGCCACCGTGC	10188
Qy	781	CGAGCACCTGAATCTCTGGGGGACCGGTCACTTCTCTTCTCCCGCCAAAAACCCAAAGAC	840
Db	10189	CGAGCACCTGAATCTCTGGGGGACCGGTCACTTCTCTTCTCCCGCCAAAAACCCAAAGAC	10248
Qy	841	ACCCTCATGATCTCCCGACCCCTGAGGTACATGCTGGTGGTGGAGCTGAGCCACGAA	900
Db	10249	ACCCTCATGATCTCCCGACCCCTGAGGTACATGCTGGTGGTGGAGCTGAGCCACGAA	10308
Qy	901	GACCTGAGGTCAAAGTTCAACTGGTACGTGGACCGCGTGGAGGTGCATAATGCCAAGACA	960
Db	10309	GACCTGAGGTCAAAGTTCAACTGGTACGTGGACCGCGTGGAGGTGCATAATGCCAAGACA	10368
Qy	961	AAGCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGTGTCAGCGTCTCTCACCGTCTG	1020
Db	10369	AAGCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGTGTCAGCGTCTCTCACCGTCTG	10428
Qy	1021	CACCAAGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCCCAAAAGCCCTCCCA	1080
Db	10429	CACCAAGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCCCAAAAGCCCTCCCA	10488
Qy	1081	GCCCCCATCGAGAAAAACATCTCAAAGCCAAAGGGCAGCCCCGAGAACCAACAGGTGTAC	1140
Db	10489	GCCCCCATCGAGAAAAACATCTCAAAGCCAAAGGGCAGCCCCGAGAACCAACAGGTGTAC	10548
Qy	1141	ACCTGTCCCCCATCCCGGATGAGCTACCAAGAACACAGTACAGCTGACTGCTGGTCTC	1200
Db	10549	ACCTGTCCCCCATCCCGGATGAGCTACCAAGAACACAGTACAGCTGACTGCTGGTCTC	10608
Qy	1201	AAAGGCTTCTATCCACGACATCGCCGTGGAGTGGGAGAGCAATGGCGACCCGGAGAAC	1260
Db	10609	AAAGGCTTCTATCCACGACATCGCCGTGGAGTGGGAGAGCAATGGCGACCCGGAGAAC	10668
Qy	1261	AACCTACAAGACCAAGCTCCCGTGTGGACTCGAGCGGCTCTTCTTCTCTACAGCAAG	1320
Db	10669	AACCTACAAGACCAAGCTCCCGTGTGGACTCGAGCGGCTCTTCTTCTCTACAGCAAG	10728
Qy	1321	CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACTCTTCTCATGCTCCGATGCAT	1380
Db	10729	CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACTCTTCTCATGCTCCGATGCAT	10788
Qy	1381	GAGGCTCTGCACAACACTACACGAGAGAGCTCTCTCTGTCTCCGGTAAATGA	1437
Db	10789	GAGGCTCTGCACAACACTACACGAGAGAGCTCTCTCTGTCTCCGGTAAATGA	10845

RESULT 12  
US-09-343-485A-2  
Sequence 2, Application US/09343485A  
Patent No. 6413777  
GENERAL INFORMATION:  
APPLICANT: REFT, MITCHELL R.  
APPLICANT: BARNETT, RICHARD S.  
APPLICANT: MC LACHLAN, KAREN R.  
TITLE OF INVENTION: NOVEL METHOD FOR



Query Match 78.5%; Score 1127.4; DB 4; Length 9209;  
Best Local Similarity 87.8%; Pred. No. 4.1e-260;  
Matches 1262; Conservative 0; Mismatches 151; Indels 24;

Qy	1	ATGGTGTGGAGCCTCACTGTCTCTCTCTTGTGCTGTGTCTACGCGTGTCCAGTGTGAG	60
Db	2401	ATGGGTGTGGAGCCTCACTGTCTCTCTCTTGTGCTGTGTCTACGCGTGTCTGTCCAG	2460
Qy	61	GTGCAACTGTGTGAGTCTGGGGAGGCTTGGTCTCAGCTGCGGGTCCCTGAGAGTCTCC	120
Db	2461	GTACAACTCGACGAGCTGGGGCTGAGCTGGTGAAGCTTGGGGCTCAGTGAAGATGTCC	2520
Qy	121	TGTGCACTCTCTGGATTACCTTCAGTGACCACTACATGTATTGGTTCGGCCAGGCTCCA	180
Db	2521	TGCAGGCTTCTGGCTACACATTTACCAAGTTACAATATGCACTGGGTAAACACAGACCT	2580
Qy	181	GGAAAGGGCCGGAATGGGTAGTGTTCATTAGAAACAACCGAACGGTGGGACACAGAA	240
Db	2581	GGTCTGGGGCTCGGAATGGATTGGAGCTATT-----TATCCGGAAATGGTGATCTTCC	2634
Qy	241	TACGCCGCTCTGTGAAAGACAGATTTCACCATCTCCAGAGATGATCCAAAGCATCGCC	300
Db	2635	TACAATCAGAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCTCCAGCAGACC	2694
Qy	301	TATCTCGAAATGAGAGCCTGAAATTCGAGGACACGGCCGCTATTACTGTACTACATCC	360
Db	2695	TACATGCAGCTCAGCAGCCTGCATCTGAGGACTCTGGGCTATTACTGTCAAGATC-	2753
Qy	361	TACATTTCATTTGTCGGGGTGGTGTCTGCTATGAGAGTTACTTCGAATTCGGGGGCGAG	420
Db	2754	-----GACTTACTAGGCGGTGACTGTGTACTTCAATGTCTGGGGCGCA	2796
Qy	421	GGCGCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA	480
Db	2797	GGACACACGGTCACCGCTCTCGAGCTAGACAAGGGCCCATCGGTCTTCCCCCTGGCA	2856
Qy	481	CCCTCTCTCAAAGACACCTCTGGGGGCAAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC	540

RESULT 10  
US-08-819-866-2  
; Sequence 2, Application US/08819866  
; Patent No. 5830698  
; GENERAL INFORMATION:  
; APPLICANT: REFF, Mitchell E.  
; APPLICANT: BARNETT, Richard Spence  
; APPLICANT: MCLACHLAN, Karen Retta  
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT  
; SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS  
; RECOMBINATION



Query Match	78.5%	Score 1127.4	DB 2	Length 9209
Best Local Similarity	87.8%	Pred. No. 4.1e-260		
Matches 1262	Conservative 0	Mismatches 151	Indels 24	Gaps 2
Qy	1	ATGGGTTGAGAGCCTCATCTTGTCTTCCCTGCTGCTGTGTACTACGGGTGTCCAGTGTGAG	60	
Db	2401	ATGGGTTGAGAGCCTCATCTTGTCTTGTCTTGTCTGTGTACTACGGGTGTCTGTGCCAG	2460	
Qy	61	GTGCAACTGTTGGAGCTGTGGGGAGGCTTGTGTCCAGCTCGGGGTCCCTGTAGAGTCTCC	120	
Db	2461	GTACAACTGCACAGCCTGGGCTGAGCTGTGTAAGCTGGGCTCAGTGAAGATGTCTCC	2520	
Qy	121	TGTGCAGTCTCTGGAAATCACCTTCAGTAGCACCATACATGATTTATGTTTCCGCCAGGCTCCA	180	
Db	2521	TGCAAGGCTTCTGGGCTCACACATTTACCAATGTAACAATATGCACTGGGTAAACAGACACCT	2580	
Qy	181	GGGAAGGGGCGCGAATGGGTAGTGTTCATTAGAAACAAACCGAACGGTGGGACCAACAGAA	240	
Db	2581	GGTGGGGCTCGAATGGATGGAGCTATT-----TATCCGGGAATGGTGATCTTCC	2634	
Qy	241	TACGCGGCTCTGTGAAGAAGATTTACCACTCTCAGAGATGATTTCCAAAGCATCGCC	300	
Db	2635	TACAATCAAAATTTCAAAGGCAAGGCCACATGTACTGCACAAATTCCTCCAGACAGCC	2694	
Qy	301	TATCTGCAAAATGAGCAGGCTGAAAAATCGAGACACGGCCGCTCTATTACTGTACTCATCC	360	
Db	2695	TACATGCACTCAGCAGCCTGCATCTGAGGACTCTCGGCTCTATTACTGTGCAAGATC-	2753	
Qy	361	TACATTTACATTTGCGGGTGGTGTCTGTATCGAGGTTACTTCGAATTTCTGGGGCCAG	420	
Db	2754	-----GACTTACTACGGCGGTGACTGTGTACTTCAATGTCTGGGGCGCA	2796	
Qy	421	GGCGGCTGGTCAACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA	480	
Db	2797	GGGACCAACCGTCAACCGTCTCTGCACTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA	2856	
Qy	481	CCCTCTCCAAGACACCTCTGGGGGACACGGCCCTCGGCTGCCTGGTCAAGGACTAC	540	
Db	2857	CCCTCTCCAAGACACCTCTGGGGGACACGGCCCTCGGCTGCCTGGTCAAGGACTAC	2916	
Qy	541	TTTCCCGAACCCGGTGAACGGTGTCTGTGNACTCAGGCGCCCTGACACAGCGGTGCACACC	600	
Db	2917	TTTCCCGAACCCGGTGAACGGTGTCTGTGNACTCAGGCGCCCTGACACAGCGGTGCACACC	2976	
Qy	601	TTCCGGGCTGTCTTACAGTCTCTCAGGACTCTACTCTCCCTCAGCAGCGTGGTGACCGTGCC	660	
Db	2977	TTCCGGGCTGTCTTACAGTCTCTCAGGACTCTACTCTCCCTCAGCAGCGTGGTGACCGTGCC	3036	





2:

Db 35 ATGGACTGGACCTGGAGGTCTCTTTTGTGGCAGCAGCTACAGGTGTCCAGTCCAG 94  
QY 61 GTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCAGCCTGGCGGGTCCCTGAGAGTCTCC 120  
Db 95 ATGCAGGTGGTGCAGTCTGGGGCTGAAGTAAGAAGACCTGGGTCTCGGTGACGGTCTCC 154  
QY 121 TGTGCAGTCTCTGGATTACCTTTCACTGACCACTACATGTATTGTTCCGCGCAGGCTCCA 180  
Db 155 TGCAGGCACTTGGAGGACCTTCAGCAACTATATGCTATCAGCTGGGTGGCAGACGGCCCT 214  
QY 181 GGGAGGGGCGGAATGGGTAGTTTATTAGAAACAAACCGAACGGTGGGACCAAGAA 240  
Db 215 GGCAAGGGCTTGGTGGATGGG-----AGGGATCATCCCTCTTTTGGTACCAACACC 268  
QY 241 TACGGCGGTCTGTGAAGACAGATTCACCACTCCAGAGATGATTCACAAAGCATCGCC 300  
Db 269 TACTCACAGAACTTCAGGGCAGAGTACGATTTACCGGGAACAAATCCACAGCACAGCC 328  
QY 301 TATCTGCAAAATGAGCAGCTGAAATCGAGACACGGCGCTTATTACTGTACTACATCC 360  
Db 329 CACATGGAGCTGACTAGCTGAGATCTGAGNACAGCGCGGTGATTACTGTGCACAGAT 388  
QY 361 TACATTTACATTTGCGGGTGGTCTGCTATATGAGGTACTTTCGAATTTCTGGGGCAG 420  
Db 389 CGCTACAGCAGCAAAATTTGACCGGGCCGGGTGGCTGCTCGACCCCTGGGGCCAG 448  
QY 421 GGGCGCTGGTCACTGCTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCGCA 480  
Db 449 GGCACCTGGTCACTGCTCTCCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCGCA 508  
QY 481 CCCTCTCTCAAGACACCTCTGGGGCACAGGGCCCTGGGCTGGTCAAGCACTAC 540  
Db 509 CCCTCTCTCAAGACACCTCTGGGGCACAGGGCCCTGGGCTGGTCAAGCACTAC 568  
QY 541 TTCCCGCAACCGGTGACGGTGTCTGGAACTCAGCGGCCCTGACAGCGGGGTGCACACC 600  
Db 569 TTCCCGCAACCGGTGACGGTGTCTGGAACTCAGCGGCCCTGACAGCGGGGTGCACACC 628  
QY 601 TTCCCGGTCTCTCAGTCTCTCAGACTCTACTCCCTCAGCGGGTGGTACCGTGGCC 660  
Db 629 TTCCCGGTCTCTCAGTCTCTCAGACTCTACTCCCTCAGCGGGTGGTACCGTGGCC 688  
QY 661 TCCAGCAGCTTGGGACCCAGACCTACATCTGCAAGTGAATCAAGCCAGCAACACC 720  
Db 689 TCCAGCAGCTTGGGACCCAGACCTACATCTGCAAGTGAATCAAGCCAGCAACACC 748  
QY 721 AAGGTGGACAAGAAAGCAGAGCCCAATCTTGTGACAAACTCAACATGCCACCGTGC 780  
Db 749 AAGGTGGACAAGAAAGTGGAGCCCAATCTTGTGACAAACTCAACATGCCACCGTGC 808  
QY 781 CCAGCACTGAATCTCTGGGGGACCGTCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840  
Db 809 CCAGCACTGAATCTCTGGGGGACCGTCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 868  
QY 841 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCTGGTGGAGCTGAGCCAGCA 900  
Db 869 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCTGGTGGAGCTGAGCCAGCA 928  
QY 901 GACCTCTGAGGTCAAGTTCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960  
Db 929 GACCTCTGAGGTCAAGTTCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 988  
QY 961 AAGCCGGGGAGGAGCAGTACACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1020  
Db 989 AAGCCGGGGAGGAGCAGTACACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1048  
QY 1021 CACGAGCTGGCTGAATGGCAAGGAGTCAAGTGAAGTCTTCAAAAGCCCTTCCA 1080  
Db 1049 CACGAGCTGGCTGAATGGCAAGGAGTCAAGTGAAGTCTTCAAAAGCCCTTCCA 1108  
QY 1081 GCCCCCATCGAAAAACCATCTTCAAAAGCCAAAGGCGCCCGGAGAACCCAGGTGTAC 1140

Db 1109 GCCCCCATCGAGAAAAACCATCTTCAAAAGCCAAAGGGAGCCCCGAGAACCCAGGTGTAC 1168  
QY 1141 ACCCTGCCCCCATCCGGGATGAGTGCACCAAGAACCCAGGTGAGCTGACCTGCTGGTC 1200  
Db 1169 ACCCTGCCCCCATCCGGGATGAGTGCACCAAGAACCCAGGTGAGCTGACCTGCTGGTC 1228  
QY 1201 AAAGGCTTCTATCCAGCAGCATCCCGTGGAGTGGGAGAGCAATGGGAGCCGAGAAC 1260  
Db 1229 AAAGGCTTCTATCCAGCAGCATCCCGTGGAGTGGGAGAGCAATGGGAGCCGAGAAC 1288  
QY 1261 AACTACAGACACCGCTCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1320  
Db 1289 AACTACAGACACCGCTCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1348  
QY 1321 CTACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGTCTCCGTGATGCAT 1380  
Db 1349 CTACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGTCTCCGTGATGCAT 1408  
QY 1381 GAGGCTTCTGCAACCACTTACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1437  
Db 1409 GAGGCTTCTGCAACCACTTACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1465

## RESULT 6

US-08-149-099C-3  
; Sequence 3, Application US/08149099C  
; Patent No. 5736137  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, Darrell R.  
; APPLICANT: HANNA, Nabil  
; APPLICANT: LEONARD, John E.  
; APPLICANT: NEWMAN, Roland A.  
; APPLICANT: REFF, Mitchell E.  
; APPLICANT: RASTETTER, William H.  
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND  
; TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED  
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/149,099C  
; FILING DATE: 03-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,891  
; FILING DATE: 12-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-014  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9209 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO





Db 9616 GTCTCAGGCGAGGGCTGGAGTGGTCTCACGTATTAGTA-----GTAGTGGTATCCC 9669  
Qy 235 ACAGATACGCGCGTCTGTGAAGACAGATTACCATCTCCAGAGATGATTCCTCAAGC 294  
Db 9670 ACATGTACGACACTCCGTGAAGGCGAGTACCATCTCCAGAGAGAACCCAGAAC 9729  
Qy 295 ATGCGCTATCTGCAATAGACAGCCTGAAATCGAGGACACGCGCGCTCTATTACTGTACT 354  
Db 9730 AACTGTCTTCAATGAACAGCCTGAGAGCTGAGGACACGCGCTGTCTATTACTGTGG 9789  
Qy 355 ACATCTCATATTTCAATTGTGCGGGGTGTGTCTGTATGAGAGTTACTTCCAAATCTGG 414  
Db 9790 AGCT-----TGACTACAGGGTCTGACTCCCTGG 9817  
Qy 415 GGCAGGCGCGCTGTCTACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCC 474  
Db 9818 GGCAGGGAGTCTGTGTACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCC 9877  
Qy 475 CTGGCACCTCTCTCAAGAGACCTCTGGGGGACACGCGGCCCTGGGCTGCTGTGCTCAAG 534  
Db 9878 CTGGCACCTCTCTCAAGAGACCTCTGGGGGACACGCGGCCCTGGGCTGCTGTGCTCAAG 9937  
Qy 535 GACTATCTTCCCGAAACGCTGTGTGTGTGAATCTCAGGGCCCTGACAGCGCGCTG 594  
Db 9938 GACTATCTTCCCGAAACGCTGTGTGTGTGAATCTCAGGGCCCTGACAGCGCGCTG 9997  
Qy 595 CACACTTCCCGGCTGCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACC 654  
Db 9998 CACACTTCCCGGCTGCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACC 10057  
Qy 655 GTGCGCTTCCAGAGCTTGGGACCCAGACCTCATCTGCAAGCTGAAATCACAGCCACG 714  
Db 10058 GTGCGCTTCCAGAGCTTGGGACCCAGACCTCATCTGCAAGCTGAAATCACAGCCACG 10117  
Qy 715 AACCAAGGTGACAAAGAACAGAGCCCAATCTTGTGAACAAACTCACATGCCCCA 774  
Db 10118 AACCAAGGTGACAAAGAACAGAGCCCAATCTTGTGAACAAACTCACATGCCCCA 10177  
Qy 775 CCGTGCCAGCACTGAATCTCTGGGGGACCGTCACTCTCTCTTCCCCCAAAACCC 834  
Db 10178 CCGTGCCAGCACTGAATCTCTGGGGGACCGTCACTCTCTCTTCCCCCAAAACCC 10237  
Qy 835 AAGACACCTCTATGATCTCTCCGAGCCCTGAGGTCACTGCGTGTGTGGACGTGAGC 894  
Db 10238 AAGACACCTCTATGATCTCTCCGAGCCCTGAGGTCACTGCGTGTGTGGACGTGAGC 10297  
Qy 895 CAGCAAGCCCTGAGTCAAGTTCAACTGTGTACGTGACGCGCTGAGGTGCATATGCC 954  
Db 10298 CAGCAAGCCCTGAGTCAAGTTCAACTGTGTACGTGACGCGCTGAGGTGCATATGCC 10357  
Qy 955 AAGCAAGCCCGGGAGGAGCAGTACAAAGCAGCAGTACCGTGTGTGTCAGCGTCTCACC 1014  
Db 10358 AAGCAAGCCCGGGAGGAGCAGTACAAAGCAGCAGTACCGTGTGTGTCAGCGTCTCACC 10417  
Qy 1015 GTCTGACACAGGACTGGCTGAATGGAAGAGGTACAAAGTGCAGAGTCTCCAAACAAAGCC 1074  
Db 10418 GTCTGACACAGGACTGGCTGAATGGAAGAGGTACAAAGTGCAGAGTCTCCAAACAAAGCC 10477  
Qy 1075 CTCCAGCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGGAGCGCCGAGAACCCACAG 1134  
Db 10478 CTCCAGCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGGAGCGCCGAGAACCCACAG 10537  
Qy 1135 GTGTACACCTTGCCTCCCATCCCGGATGAGTCAACCAAGAACAGGTCAGCTGACTGC 1194  
Db 10538 GTGTACACCTTGCCTCCCATCCCGGATGAGTCAACCAAGAACAGGTCAGCTGACTGC 10597  
Qy 1195 CTGTCAAAGGCTTCTATCCAGCAGCATCCCGTGTGAGTGGAGAGCAATGGGCGCCG 1254  
Db 10598 CTGTCAAAGGCTTCTATCCAGCAGCATCCCGTGTGAGTGGAGAGCAATGGGCGCCG 10657  
Qy 1255 GAGCAAACTACAGACACGCTCCCGTGTGTGACTCCGACCGCTCTTCTTCTCTAC 1314

Db 10658 GAGAAACACTAAGACCACCGCTCCCGTCTCGAGCTCCGACGGCTCTTCTTCTCTAC 10717  
Qy 1315 AGCAAGCTCACCGTGGACAAAGACAGGTGCACAGAGGGAACGTCTTCTCATGCTCGTG 1374  
Db 10718 AGCAAGCTCACCGTGGACAAAGACAGGTGCACAGAGGGAACGTCTTCTCATGCTCGTG 10777  
Qy 1375 ATGATGAGGCTTGCAACAACCACTACACGAGAGGCTCTCCCTGTCTCCGGGTAAA 1434  
Db 10778 ATGATGAGGCTTGCAACAACCACTACACGAGAGGCTCTCCCTGTCTCCGGGTAAA 10837  
Qy 1435 TGA 1437  
Db 10838 TGA 10840  
  
RESULT 3  
US-08-157-101A-6  
; Sequence 6, Application US/08157101A  
; Patent No. 5808032  
; GENERAL INFORMATION:  
; APPLICANT: KURIHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU  
; APPLICANT: TSURUOKA, NOBUO  
; APPLICANT: ARIMA, KENJI  
; APPLICANT: NISHIHARA, TATSURO  
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION  
; TITLE OF INVENTION: PLASMIDS THEREFOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08157,101A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TITUS, MARLANA K  
; REGISTRATION NUMBER: 35843  
; REFERENCE/DOCKET NUMBER: 9437/204199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3711  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 CUCH  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1576 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-157-101A-6

Query Match 80.4%; Score 1155.8; DB 1; Length 1576;  
Best Local Similarity 90.1%; Pred. No. 4.1e-267;  
Matches 1270; Conservative 0; Mismatches 112; Indels 27; Gaps 2;  
  
Qy 29 TTGTGCGCTGTGTACGCGTGTCCAGTGTGAGGTGCAACTCGTGGAGTCTGGGGAGGCT 88  
Db 13 TCGTTGGCCTTTAAGAGGTGTCCAGTGTGAGTGCAGTGTGGAGTCTGGGGAGGCG 72  
Qy 89 TGGTCCAGCCTGGCGGTCCTGAGAGTCTCTGTGCAAGTCTCTGGAATTCACCTTCAGTG 148  
Db 73 TGGTCCAGCCTGGGAGGTCCCTGAGACTCTCTGTGACGCTCTGGATTTCACCTTCAGTA 132



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 5, 2003, 19:47:34 ; Search time 65.4298 Seconds  
(without alignments)  
6735.375 Million cell updates/sec

Title: US-09-758-173-7

Perfect score: 1437

Sequence: 1 ATGGGTGAGGCTCATCTT.....CCTGCTCCGGGTAATGA 1437

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/prodata/1/ina/PCUS\_COMB.seq:\*

6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1437	100.0	1437	3	US-08-487-550-7
2	1177.8	82.0	19040	4	US-09-343-485A-3
3	1155.8	80.4	1576	1	US-08-157-101A-6
4	1142	79.5	1350	1	US-08-157-101A-9
5	1131.8	78.8	1617	2	US-08-378-939-9
6	1127.4	78.5	9209	1	US-08-149-099C-3
7	1127.4	78.5	9209	1	US-08-476-275-2
8	1127.4	78.5	9209	2	US-08-478-967A-3
9	1127.4	78.5	9209	2	US-08-475-815B-3
10	1127.4	78.5	18986	2	US-08-819-866-2
11	1127.4	78.5	18986	4	US-09-023-715-2
12	1127.4	78.5	18986	4	US-09-343-485A-2
13	1120.6	78.0	8120	3	US-09-027-449-68
14	1120.6	78.0	8120	3	US-09-026-985-68
15	1120.6	78.0	8120	4	US-09-121-952A-68
16	1118.2	77.8	8120	4	US-09-234-340A-68
17	1118.2	77.8	1428	1	US-08-488-376-19
18	1118.2	77.8	1428	2	US-08-634-223-19
19	1118.2	77.8	1428	2	US-08-634-224-19
20	1118.2	77.8	1428	2	US-08-634-400-19
21	1118.2	77.8	1428	2	US-08-635-878-19
22	1118.2	77.8	1428	2	US-08-770-057-19
23	1118.2	77.8	1428	4	US-09-335-697B-19
24	1118.2	77.8	1428	4	US-09-335-697B-19
25	1117.2	77.5	1431	3	US-08-487-550-3
26	1113.4	77.5	1428	1	US-08-488-376-17
27	1113.4	77.5	1428	2	US-08-634-223-17

Query Match 100.0%; Score 1437; DB 3; Length 1437;

## ALIGNMENTS

### RESULT 1

US-08-487-550-7

; Sequence 7, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1437 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1437

; FEATURE:

; NAME/KEY: mat.peptide

; LOCATION: 1..1437

US-08-487-550-7















Barnett RS, McLachlan KR, Reff ME;

WPI; 1998-521229/44.

**Site specific integration of DNA in mammals for expressing, e.g. immunoglobulins - comprises homologous recombination using selectable marker and target plasmids.**

Example 1; Fig 10; 114pp; English.

This is the nucleotide sequence of novel target plasmid Mandy. The plasmid includes an inactivated murine dihydrofolate reductase (DHFR) gene, the *Escherichia coli* beta-galactosidase gene, baculovirus DNA, a cassette comprising the promoter and enhancer elements from cytomegalovirus and SV40 virus, the *E. coli* beta-glucuronidase (GUS) gene, firefly luciferase gene, an inactivated *Salmonella typhimurium* histidinol dehydrogenase (*hisD*) gene and transposon *tn5* neomycin phosphotransferase (*neo*) gene sequences, in a pBR-derived backbone, and also an anti-human CD23 IgE receptor human gamma-1 monoclonal antibody 5S8 gene. The invention provides a novel method for integrating a desired exogenous DNA at a target site within the genome of a mammalian cell via homologous recombination. This involves transfecting the cell with a 'marker plasmid' such as Desmond (see AAV61792), which contains a unique sequence that is foreign to the mammalian cell genome and which provides a substrate for homologous recombination, followed by transfection with a 'target plasmid', such as Mandy or Molly (see AAV61793), containing a sequence which provides for homologous recombination with the unique sequences contained in the marker plasmid, and further comprising a desired DNA that is to be integrated into the mammalian cells, typically an immunoglobulin or other secreted mammalian glycoprotein. The homologous recombination system utilises the neo gene as a dominant selectable marker. The neo gene is split into 3 exons. Exon 3 is present on the marker plasmid and becomes integrated into the host cell genome upon integration of the marker plasmid into the mammalian cells. Exons 1 and 2 are present on the targeting plasmid, and are separated by an intron into which at least one gene of interest is cloned. Homologous recombination of the targeting vector with the integrated marking vector results in correct splicing of all 3 exons of the neo gene and expression of a functional neo protein. The method is applicable to all mammalian cells, and can be used to express any type of recombinant protein. The use of a triply spliced selectable marker means that all selected colonies arise from homologous recombination. In addition, the number of colonies that need to be screened to identify high producer clones is reduced. An amplifiable gene can be inserted on integration of the marking vector, so that when a gene is targeted to this site, the gene is further enhanced by gene amplification.

Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other;

Query Match	82.3%	Score 1182.2	DB 19	Length 19035
Local Similarity	90.8%	Pred. No. 1.1e-226		
Mismatches 1310	Conservative	0	Mismatches 88	Indels 45
				Gaps

1 ATGGGTTGGAGCCTCATCTTGCTTCTTCCTTGTCCGTGTTGCTACGCCGTGCCAGTGTGAG 60  
|||||  
9432 ATGGGTTGGAGCCTCATCTTGCTTCTTCCTTGTCCGTGTTGCTACGCCGTGCCAGTGTGCGAG 9491

61 GTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGACTCTCC 120  
|||||  
9492 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTCC 9551

121 TTGTCAGTCTCTG-----GATTACCTTCAGTGACCACATCATGTATGGTTCGCCAG 174  
|||||  
9552 TGCGCAGCTCCGGGTCAGGTCACCTTCAATACTACTACATGGATGGGTCGCCAG 9611

175 .GTCCAGGGAAGGGGCCGGAATGGGTAGTGTTCATTAGAAACAAACCGAACGGTGGGACA 234  
|||||  
9612 GTCCAGGCGAGGGGTGGAGTGGGTCTCACGTAATAGTA-----GTAGTGGTCATATCC 9665  
|||||

Qy	1381	GAGGCTCTGCACACACACTACACGACAGAGACCTCTCCCTGTCTCTCCGGGTAATGA	1431
Db	1472	GAGGCTCTGCACAAACCACTACACACAGAGAGCCCTCTCCCTGTCTCTCCGGGTAATGA	1528
RESULT 11			
AAV61794			
ID	AAV61794	standard; DNA; 19035 BP.	
XX	AC	AC	
XX	AAV61794;		
XX	DT	DT	
XX	07-JUN-1999	(first entry)	
XX	DE	Traget plasmid Mandy containing anti-CD23 gene.	
XX	DE		
KW	Mandy;	target plasmid; gene integration; gene amplification;	
KW	homologous recombination; vector;	neomycin phosphotransferase;	
KW	neo gene;	selectable marker; immunoglobulin; CD23; 588; human; ss.	
OS	Chimeric - Mus sp.		
OS	Chimeric - Escherichia coli.		
OS	Chimeric - Baculovirus.		
OS	Chimeric - Cytomegalovirus.		
OS	Chimeric - Rhesus macaque polyoma virus.		
OS	Chimeric - Photinus sp.		
OS	Chimeric - Salmonella typhimurium.		
OS	Chimeric - Homo sapiens.		
XX	Key	Location/Qualifiers	
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FT	FT	/*note=	"this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"
FT	FT		
FT	misc_feature	721	
FT	FT	/*tag=	b
FT	FT	/*note=	"this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"
FT	FT		
FT	misc_feature	2941	
FT	FT	/*tag=	c
FT	FT	/*note=	"this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"
FT	FT		
FT	misc_feature	3301	
FT	FT	/*tag=	d
FT	FT	/*note=	"this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"
FT	FT		
FT	misc_feature	4261	
FT	FT	/*tag=	e
FT	FT	/*note=	"this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"
FT	FT		
FT	misc_feature	4621..4622	
FT	FT	/*tag=	f
FT	FT	/*note=	"these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence"
FT	FT		
FT	misc_feature	8161	
FT	FT	/*tag=	g
FT	FT		







QY 121 TGTGAGTCTCTGATTCACCTTCAGTGACCACTACATGTTATGTTCCGCCAGGCTCA 180  
Db 124 TGTGAGCTCTTGATTCACCTTTAGCACTATGCGATGGTTCGCCAGGCTCCA 183  
QY 181 GGAAGGGGCGGAAATGGGTAGTCTTTCATTAGAAACAAACCGAATGGGAGCAACAGAA 240  
Db 184 GGAAGGGGCTGGAGTGGGTCTCAGCTATTAG-----TGCTAGTGGTCAATGACCATAT 237  
QY 241 TAGCCGCGTCTGTGAAGACAGATTACCATCTCCAGAGATGATTCAAAAGCATCGCC 300  
Db 238 TTGGCAGACTCCGTGAAGGCGCGGTTCACCATCTCCAGAGACAAATTCGAAGAACACGCTG 297  
QY 301 TATCTGCAATAGAGCAGCTTGAAATCGAGGACACGGCCGCTTATTAATGTTACTACATCC 360  
Db 298 TATCTGCAATAGAGCAGCTTGAGAGCGGAGGACACGGCCGCTATTAATGTTACTGTCGA----- 352  
QY 361 TACATTTCAATTTGTCGGGGTGTGTCGTATGAGGTTACTTCGAAATTCGGGGCCAG 420  
Db 353 -AAGATCGAGAGGTTACTATGATAGTTGTACTTAATGAGGCTTTGACTACTGGGCCAG 411  
QY 421 GGCGCCCTGTGTACCCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCGCTGGCA 480  
Db 412 GGAACCGGGTCACTCTCTCCGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCA 471  
QY 481 CCTCTCTCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGCTGTCAAGGACTAC 540  
Db 472 CCTCTCTCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGCTGTCAAGGACTAC 531  
QY 541 TTCCCGGACCGGTGAGCGTGTGTGGAATCACTAGGGCCCTGACAGGGCGGTGACAC 600  
Db 532 TTCCCGGACCGGTGAGCGTGTGTGGAATCACTAGGGCCCTGACAGGGCGGTGACAC 591  
QY 601 TTCCCGGCTGTCTCAGAGCTCTCAGAGCTCTACTCCCTCAGCAGCGTGTGACCGTCCC 660  
Db 592 TTCCCGGCTGTCTCAGAGCTCTCAGAGCTCTACTCCCTCAGCAGCGTGTGACCGTCCC 651  
QY 661 TCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCAAAAGCCAGCAACACC 720  
Db 652 TCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCAAAAGCCAGCAACACC 711  
QY 721 AAGGTGGACAAGAAAGCAGAGCCCAAAATCTGTGACAAATCTCACAATGCCACCGTGC 780  
Db 712 AAGGTGGACAAGAGAGTGTAGGCCCAAAATCTGTGACAAATCTCACAATGCCACCGTGC 771  
QY 781 CCAGCACCTGAATCTCTGGGGGACCGTCAGTCTTCTCTTCCCGCCAAAACCCAAAGGAC 840  
Db 772 CCAGCACCTGAATCTCTGGGGGACCGTCAGTCTTCTCTTCCCGCCAAAACCCAAAGGAC 831  
QY 841 ACCCTCATGATCTCCGGACCCCTGAGTCAATCGGTGGTGGAGCGTGAGCCACGAA 900  
Db 832 ACCCTCATGATCTCCGGACCCCTGAGTCAATCGGTGGTGGAGCGTGAGCCACGAA 891  
QY 901 GACCCTGAGGTCAAGTTCACTGGTACGTGGAGCGGCTGAGGTGCAATGTCGAAGACA 960  
Db 892 GACCCTGAGGTCAAGTTCACTGGTACGTGGAGCGGCTGAGGTGCAATGTCGAAGACA 951  
QY 961 AAGCCGCGGAGGAGCAGTACAAAGCAGTACCGTGTGGTCAAGCTCTCACCCTCTCTG 1020  
Db 952 AAGCCGCGGAGGAGCAGTACAAAGCAGTACCGTGTGGTCAAGCTCTCACCCTCTCTG 1011  
QY 1021 CACCAAGGACTGCTCAATGGCAAGAGTACAAGTCAAGGTCTCAACAAAGCCCTCCCA 1080  
Db 1012 CACCAAGGACTGCTCAATGGCAAGAGTACAAGTCAAGGTCTCAACAAAGCCCTCCCA 1071  
QY 1081 GCGCCCATCGAGAAACCATCTCCAAAGCAGGAGCGCCGAGACACCAAGTGTAC 1140  
Db 1072 GCGCCCATCGAGAAACCATCTCCAAAGCAGGAGCGCCGAGACACCAAGTGTAC 1131  
QY 1141 ACCCTGCCCCCATCCCGGATGAGTGACCAAGAACCAAGGTGACCTGCTGGTC 1200  
Db 1132 ACCCTGCCCCCATCCCGGAGGAGATGACCAAGAACCAAGGTGACCTGCTGGTC 1191

QY 1201 AAAGCTTCTATCCAGGACATCGCGTGGAGAGCAATGGCAGCCCGGAGAAC 1260  
Db 1192 AAAGCTTCTATCCAGGACATCGCGTGGAGAGCAATGGCAGCCCGGAGAAC 1251  
QY 1261 AACTACAAGACCAAGCTCCGCTGCTGACTCCGACGGCTCTTCTCTCTACAGCAAG 1320  
Db 1252 AACTACAAGACCAAGCTCCGCTGCTGACTCCGACGGCTCTTCTCTCTATAGCAAG 1311  
QY 1321 CTACCGTGGACAAGAGCAGTGGCAGCAGGGAAACGTCTTCTCATGCTCCGTCATGCAT 1380  
Db 1312 CTACCGTGGACAAGAGCAGTGGCAGCAGGGAAACGTCTTCTCATGCTCCGTCATGCAT 1371  
QY 1381 GAGGCTCTGCACACCACTACACGACAGAGGCTCTCCCTGTCTCCGGTAAATGA 1437  
Db 1372 GAGGCTCTGCACACCACTACACGACAGAGGCTCTCCCTGTCTCCCGGTAATGA 1428

RESULT 9  
AAS22593  
ID AAS22593 standard; cDNA; 1644 BP.  
XX  
AC AAS22593;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human cDNA encoding a novel human protein #159.  
XX  
KW Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory;  
KW immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;  
KW anticonvulsant; antiarthritic; cerebrotective; antifungal; antiviral;  
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
KW thrombolytic; immunogen antibody; gene therapy; neurological disorder;  
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
KW tissue regeneration; immune disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200155437-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-US02623.  
XX  
PR 25-JAN-2000; 2000US-0491404.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI; 2001-451939/48.  
XX  
PS P-PSDB; AAU14288.  
PT Isolated polypeptides useful for treating anti-inflammatory diseases,  
PT nervous system disorders, and for regenerating bone and cartilage -  
XX  
PS Claim 1; Page 387-389; 894pp; English.  
XX  
CC The invention relates to polynucleotides encoding novel human  
CC proteins or their active domains. The polypeptides, polynucleotides and  
CC antibodies raised against the polypeptides are used in a method of  
CC treatment of a mammal and prevention of disorders caused by the aberrant  
CC protein expression or activity. The polypeptides can be used as  
CC molecular weight markers, food supplements, and in antibody production.  
CC The polypeptides are used to identify compounds which bind to the  
CC polypeptides. Polynucleotides of the invention are used as probes and  
CC primers, for sequencing, for chromosome or gene mapping, in the  
CC production of recombinant proteins, and in generating anti-sense DNA or  
CC RNA and in gene therapy. Polypeptides of the invention can be used to  
CC target drugs to a tumour, in assays to determine biological activity, to  
CC raise antibodies/elicit an immune response, to determine quantitative  
CC protein levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,

Dd 1511 GAGGCTCTGCACACCACTACACGACAGAGCCTCTCCCTGTCTCYCCGGGTAATGA 1567

RESULT 8  
AAK98701  
ID AAK98701 standard; cDNA; 1430 BP.  
XX AC  
XX AAK98701;  
XX AC  
XX 07-MAY-2002 (first entry)  
XX DE  
XX cDNA of the heavy chain of the monoclonal antibody from clone JA.  
XX DE  
XX HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain;  
KW human monoclonal rabies virus neutralising antibody; immunoglobulin;  
KW light chain; central nervous system; CNS; prophylactic therapy; clone JA;  
KW ss.  
XX XX  
XX Homo sapiens.  
OS XX  
XX Key Location/Qualifiers  
FH 4..1428  
CDS /\*tag= a  
FT /product= "JA clone heavy chain protein"  
FT FT  
XX WO2001188132-A2.  
PN PN  
PD 22-NOV-2001.  
XX XX  
PF 04-MAY-2001; 2001WO-US14468.  
XX XX  
PR 16-MAY-2000; 2000US-204518P.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX XX  
FI Hooper DC, Dietzschold B;  
XX XX  
DR WPI; 2002-062381/08.  
DR P-PSDB; AAO14065.  
XX XX  
PT Novel isolated human monoclonal rabies virus neutralising antibody  
PT useful for treating individual exposed to rabies virus and for  
PT preventing spread of rabies virus to central nervous system -  
XX XX  
PS Claim 2; Page 22; 25pp; English.  
XX XX  
CC This polynucleotide sequence represents the cDNA of the heavy chain of  
CC the monoclonal antibody from clone JA. The invention relates to an  
CC isolated human monoclonal rabies virus neutralising antibody (virucide)  
CC derived from cDNA clones encoding the antibody heavy and light chains  
CC expressed in heterologous expression systems and purified away from  
CC deleterious contaminants. The invention provides a fused gene encoding a chimeric  
CC chimeric immunoglobulin light chain and a fused gene encoding a chimeric  
CC immunoglobulin heavy chain. The antibody of the invention is useful for  
CC treating an individual exposed to a rabies virus by administering to the  
CC individual a therapeutically effective amount of the antibody, and  
CC preventing a spread of the rabies virus to the central nervous system  
CC (CNS). The antibody of the invention provides a safe and efficacious post  
CC exposure prophylactic therapy for individuals exposed to a rabies virus.  
XX XX  
SQ Sequence 1430 BP; 326 A; 438 C; 396 G; 270 T; 0 other;

Query Match 82.5%; Score 1185; DB 24; Length 1430;  
Best Local Similarity 90.1%; Pred. No. 2.4e-227;  
Matches 1295; Conservative 0; Mismatches 130; Indels 12; Gaps 2

Qy 1 ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTGCGTGTGCTACGCGTGTCAGGTGAG 60  
Dd 4 ATGCAATTGGGCTGAGCTGGGCTTTTCTTGTGGGTATTTTAAAAGGTGTCAGGTGAG 63  
Qy 61 GTGCCAATCGGTGAGCTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTCGAGAGTCTCC 120  
Db 64 GTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC 123